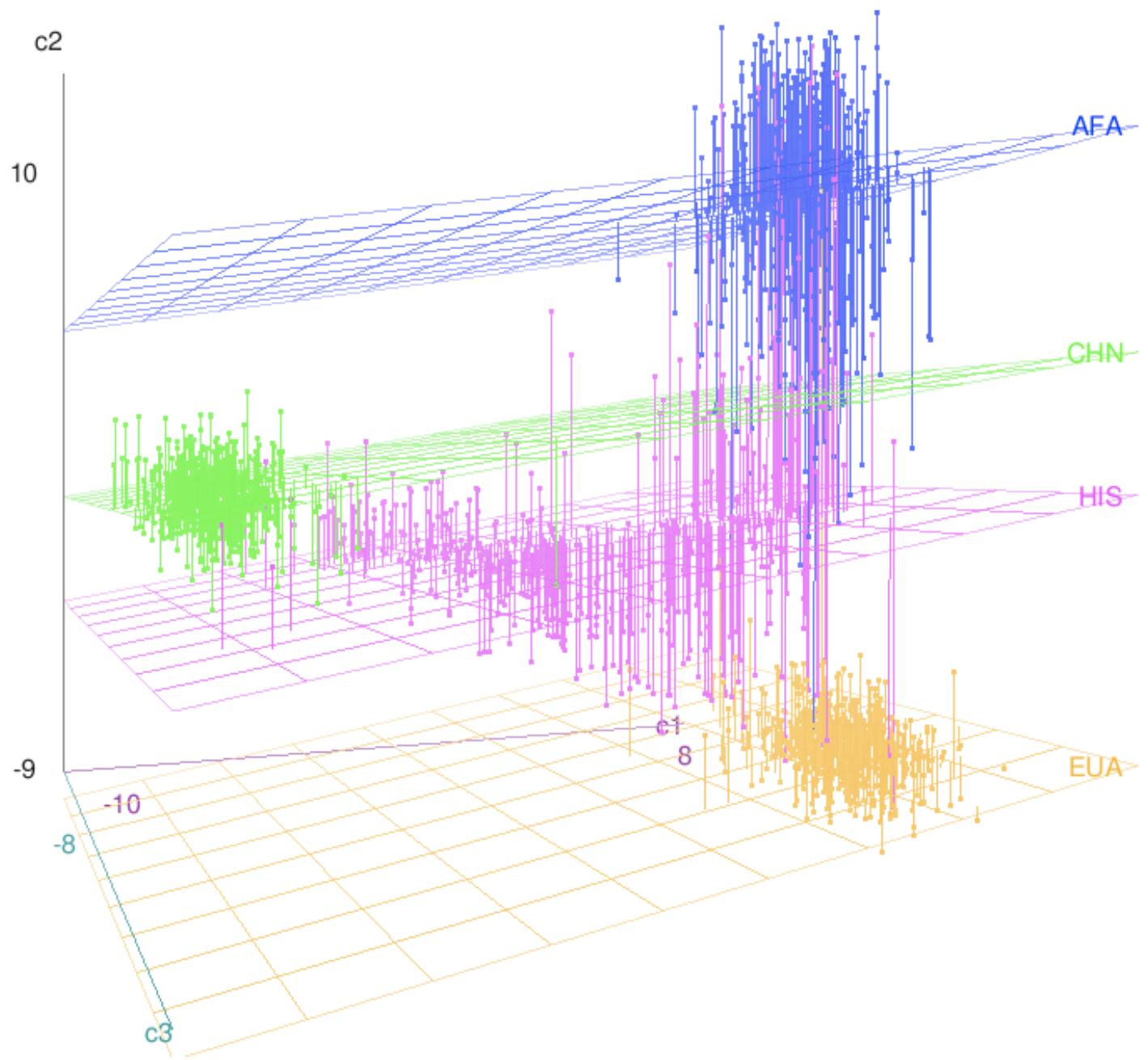
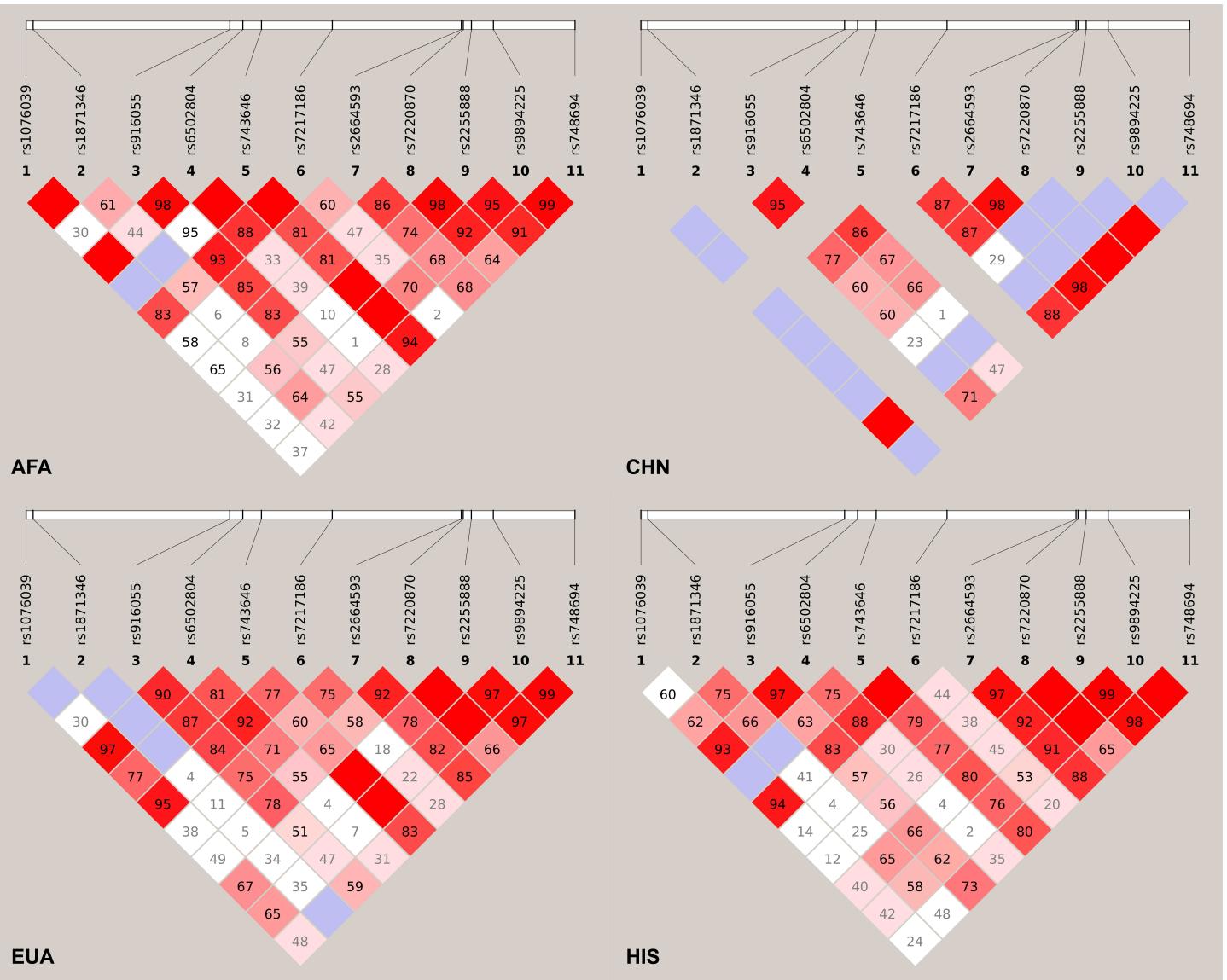


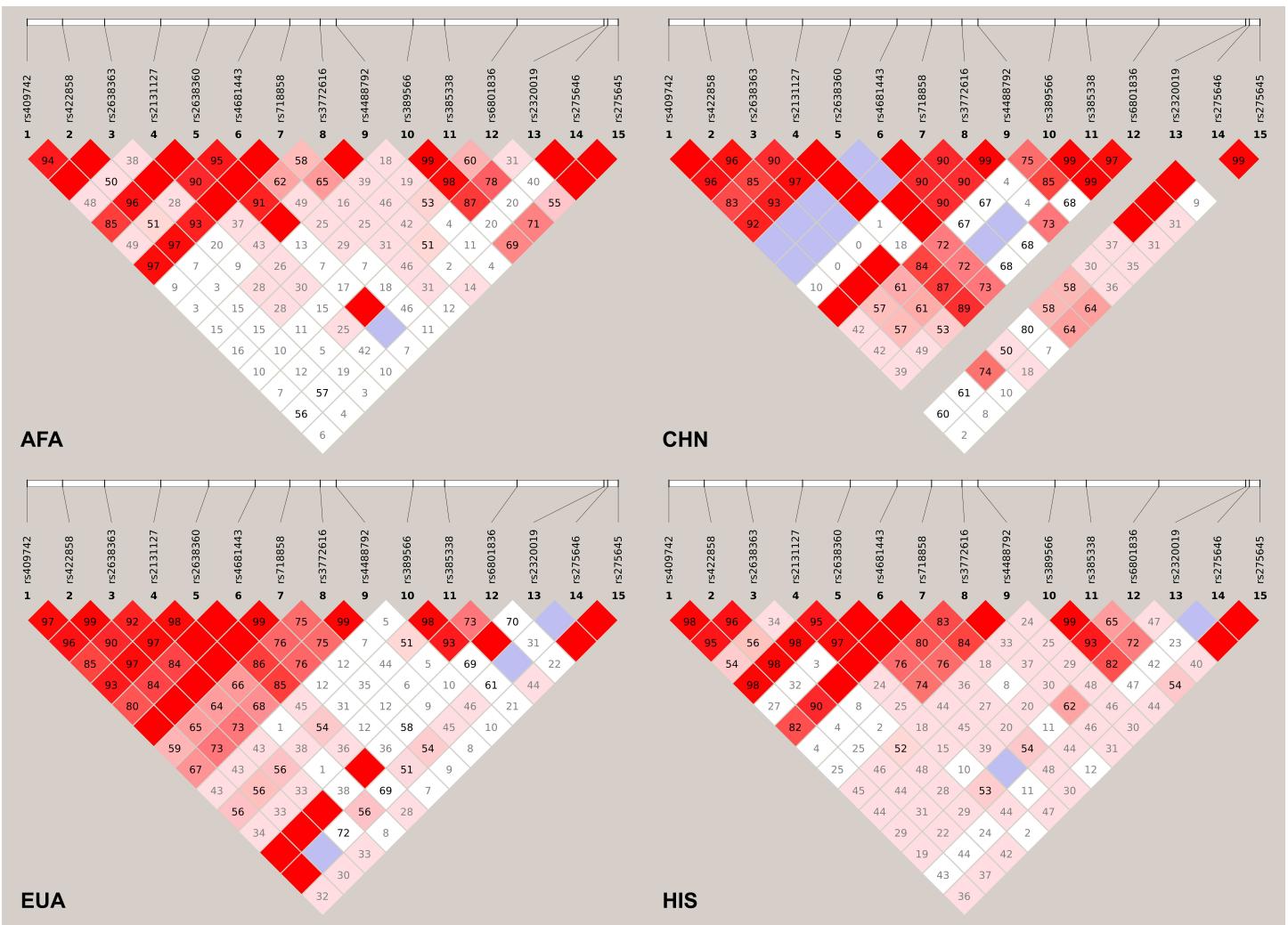
Supplemental Material, Figure 1: Log quantile-quantile p value plot of 115 tests for SNP-roadway proximity interactions on LVM. Model 1 (minimally-adjusted model) contains each tagSNP, proximity to roadway categories, interaction terms between SNP and proximity, study site, age, gender, height, weight, and the principal components of ancestry-informative markers. Model 2 contains covariates from Model 1, plus diabetes, lipids, education, income, alcohol use, and physical activity. Model 3 adds smoking to Model 2. Model 4 adds blood pressure to Model 3. Model 5, the fully adjusted model, adds medication usage (ACE inhibitors, angiotensin receptor blockers, diuretics, beta-blockers, lipid-lowering medications, aspirin, non-steroidal anti-inflammatories, and COX inhibitors) to Model 4. Each point represents one SNP\*proximity interaction test. Labeled points represent interactions for which observed p values are smaller in magnitude than expected by chance.



Supplemental Material, Figure 2: First three principal components of ancestry-informative markers, by self-reported race, Multi-Ethnic Study of Atherosclerosis. AFA, African American; CHN, Chinese; EUA, European American; HIS, Hispanic.



Supplemental Material, Figure 3: Linkage disequilibrium map for ALOX15 tagSNPs genotyped, stratified by race, Multi-Ethnic Study of Atherosclerosis. AFA, African American; CHN, Chinese; EUA, European American; HIS, Hispanic.



Supplemental Material, Figure 4: Linkage disequilibrium map for AGTR1 tagSNPs genotyped, stratified by race, Multi-Ethnic Study of Atherosclerosis. AFA, African American; CHN, Chinese; EUA, European American; HIS, Hispanic.

Gene	tagSNP	SNPs				Haplotypes			
		Position	Major allele	Minor allele	MAF <sup>a</sup>	Missing	Haplotype ID <sup>c</sup>	Structure <sup>b</sup>	Frequency <sup>a</sup>
ACE	rs4291	58907926	T	A	35%	0.0%	ACE-A	TGCGAGAAGGGAGAAGA	25%
	rs4295	58910030	G	C	37%	0.0%	ACE-B	ACCAAGGAAAGATGGG	12%
	rs4303	58911555	C	A	2%	0.2%	ACE-C	ACCAAGGAAAGAAAGA	7%
	rs4305	58911961	A	G	50%	0.1%	ACE-D	TGCGAGAAGGGAGTGGG	4%
	rs4309	58913655	G	A	44%	0.1%	ACE-E	TGCGAGAAGGGAGTGGG	4%
	rs4311	58914495	G	A	37%	0.0%	ACE-F	ACCAAGGAGAAGAAGA	3%
	rs4316	58916041	A	G	49%	0.0%	ACE-G	TGCGAGGAAAGATGGG	3%
	rs4351	58923464	A	G	47%	0.0%	ACE-others		42%
	rs4353	58924154	A	G	50%	0.0%			
	rs4359	58926075	G	A	46%	0.2%			
	rs4362	58927493	G	A	45%	0.2%			
	rs4363	58928224	A	G	46%	0.1%			
	rs4461142	58931780	G	A	37%	0.1%			
	rs4459610	58938452	A	T	46%	0.2%			
ADRB2	rs8066276	58942997	A	G	42%	0.8%			
	rs4277404	58946485	G	A	2%	0.5%			
	rs4968591	58951850	A	G	27%	0.0%			

ADRB2	rs12654778	148185934	G	A	34%	0.0%	ADRB2-A	GGGG	29%
	rs11168070	148186120	G	C	22%	0.0%	ADRB2-B	AGAC	28%
	rs1042713	148186633	G	A	47%	0.2%	ADRB2-C	GCGC	22%
	rs1042719	148187640	C	G	37%	3.2%	ADRB2-D	GGAC	13%
							ADRB2-E	AGAG	6%
							ADRB2-others		3%

AGT	rs7536290	228903325	A	G	26%	0.0%	AGT-A	AAGCGAAGA	29%
	rs943580	228903667	G	A	31%	0.0%	AGT-B	AGGAGGGAG	14%
	rs3789670	228910337	G	A	16%	0.0%	AGT-C	AGAAGGGGA	14%
	rs3789671	228910423	C	A	34%	0.3%	AGT-D	GGGCAGGGA	13%
	rs2478545	228910744	G	A	34%	0.0%	AGT-E	GGGCAGGAG	9%
	rs699	228912417	G	A	32%	0.0%	AGT-F	AGGCAGGGA	8%
	rs2148582	228916422	G	A	32%	0.0%	AGT-others		13%
	rs7549009	228921694	G	A	30%	0.1%			
	rs1326886	228926383	A	G	26%	0.0%			

AGTR1	rs409742	149895055	A	G	18%	0.1%	AGTR1-A	AAGGAGGGAGAAGA	19%
	rs422858	149898174	A	C	17%	0.0%	AGTR1-B	AAGAAGGGAGAAGA	11%
	rs2638363	149901883	G	A	20%	0.0%	AGTR1-C	AAGGAGGGAGAAGG	8%
	rs2131127	149906833	G	A	44%	0.0%	AGTR1-D	AAGAAAAAAAGAAGA	4%
	rs2638360	149911046	A	G	10%	0.0%	AGTR1-E	AAGAAAAGAACCGGG	3%
	rs4681443	149915159	G	A	27%	0.0%	AGTR1-F	GCAGGGGGGTGAGG	3%
	rs718858	149918202	G	A	16%	0.0%	AGTR1-others		52%
	rs3772616	149920881	G	A	36%	0.5%			
	rs4488792	149922293	G	A	32%	0.0%			
	rs389566	149929072	A	T	33%	0.0%			
	rs385338	149931846	G	C	26%	0.0%			
	rs6801836	149938227	A	G	23%	0.0%			
	rs2320019	149945884	A	G	12%	0.0%			
	rs275646	149946212	G	A	7%	0.0%			
	rs275645	149947144	A	G	50%	0.0%			

ALOX15	rs1076039	4472520	A	T	8%	0.0%	ALOX15-A	AAGAAGGCAGA	23%
	rs1871346	4472833	A	G	5%	0.0%	ALOX15-B	AAAGAAGCAGG	16%
	rs916055	4481583	A	G	32%	0.1%	ALOX15-C	AAAGAACAAAGA	9%
	rs6502804	4482162	G	A	47%	0.1%	ALOX15-D	AAAGAGGCAG	5%
	rs743646	4482990	A	G	5%	0.0%	ALOX15-E	TAAAAGGCAG	4%
	rs7217186	4486141	G	A	47%	0.3%	ALOX15-F	AAAGAACAGCA	4%
	rs2664593	4491881	G	C	19%	0.0%	ALOX15-G	AAAGAACAGCAG	4%
	rs7220870	4491967	C	A	21%	0.0%	ALOX15-H	AAAAAAGGCAG	4%
	rs2255888	4492330	A	G	26%	0.3%	ALOX15-I	AAAGGACAAGA	3%
	rs9894225	4493308	G	A	23%	0.0%	ALOX15-J	AGAGAGGCAG	3%
	rs748694	4496938	A	G	49%	0.0%	ALOX15-others		25%

EDN1	rs3087459	12397625	A	C	20%	0.0%	EDN1-A	AGAC	39%
	rs1476046	12401207	G	A	23%	0.0%	EDN1-B	AGGC	34%
	rs1630736	12403973	G	A	40%	0.0%	EDN1-C	CAGA	16%
	rs5370	12404241	C	A	22%	0.1%	EDN1-D	AAGA	6%
							EDN1-E	CGGC	3%

Gene	tagSNP	SNPs				Haplotypes			
		Position	Major allele	Minor allele	MAF <sup>a</sup>	Missing	Haplotype ID <sup>c</sup>	Structure <sup>b</sup>	Frequency <sup>a</sup>
GRK4	rs2488813	2934186	A	T	24%	0.9%	GRK4-A	ACAGGAGCAAGAACACGA	28%
	rs1056094	2937396	C	G	32%	0.1%	GRK4-B	ACAGGAGCAAGAAGGACGA	11%
	rs2185886	2941295	A	G	41%	0.0%	GRK4-C	ACAGGAGCAAGAAGAGAAG	10%
	rs3021140	2948828	G	A	31%	0.1%	GRK4-D	TGGAGTAAGGAACAGGAAG	10%
	rs2105380	2952727	G	A	3%	0.0%	GRK4-E	ACAGGAGCAAGAAGGGAAAG	6%
	rs1419046	2955847	A	T	32%	0.1%	GRK4-F	TGGAGTAAGGAACAAGAAG	6%
	rs2488815	2958434	G	A	39%	0.0%	GRK4-G	ACGGGAACAAAACAGACGA	4%
	rs2960306	2960297	C	A	32%	0.1%	GRK4-others		25%
	rs2471337	2964784	A	G	30%	0.0%			
	rs2960298	2971725	A	G	31%	0.1%			
	rs1024323	2975841	G	A	38%	0.0%			
	rs6846128	2983378	A	G	5%	0.0%			
	rs2488806	2990734	A	C	40%	0.0%			
	rs2471327								

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 1	A	rs389566	major	-2.879995	0.0138805	0.035514	-5.486563	-0.2015413	0.0010037	0.0555895
AGTR1	Model 1	T	rs389566	minor	6.336318	0.0208917	0.0033501	2.0701	10.78085	0.0010037	0.0555895
AGTR1	Model 1	A	rs6801836	major	-2.541081	0.012786	0.0443748	-4.953068	-0.0678856	0.0006816	0.0555895
AGTR1	Model 1	G	rs6801836	minor	8.601004	0.0262708	0.0017347	3.150669	14.33932	0.0006816	0.0555895
AGTR1	Model 2	A	rs389566	major	-2.889629	0.0139281	0.0355201	-5.50475	-0.2021348	0.0013782	0.0792465
AGTR1	Model 2	T	rs389566	minor	6.087198	0.0209921	0.0049748	1.810955	10.54305	0.0013782	0.0792465
AGTR1	Model 2	A	rs6801836	major	-2.602486	0.0128308	0.0401215	-5.021279	-0.1220941	0.0007178	0.0792465
AGTR1	Model 2	G	rs6801836	minor	8.498069	0.0263422	0.0020145	3.0385	14.24692	0.0007178	0.0792465
AGTR1	Model 3	A	rs389566	major	-2.837958	0.0138986	0.038575	-5.449006	-0.1548055	0.0016726	0.0961745
AGTR1	Model 3	T	rs389566	minor	5.963228	0.0209587	0.0058216	1.698628	10.40666	0.0016726	0.0961745
AGTR1	Model 3	A	rs6801836	major	-2.547106	0.0128082	0.0442344	-4.963082	-0.0697121	0.0009808	0.0961745
AGTR1	Model 3	G	rs6801836	minor	8.248896	0.0263183	0.0026633	2.806672	13.97921	0.0009808	0.0961745
AGTR1	Model 4	A	rs6801836	major	-1.952968	0.0121348	0.1044094	-4.257376	0.4069036	0.0018643	0.1615727
AGTR1	Model 4	G	rs6801836	minor	7.702175	0.0249345	0.0029929	2.565234	13.0964	0.0018643	0.1615727
ALOX15	Model 4	G	rs2664593	major	-1.482974	0.0114776	0.1933074	-3.674441	0.7583498	0.0044107	0.1911303
ALOX15	Model 4	C	rs2664593	minor	8.336904	0.0289973	0.0058594	2.351427	14.67241	0.0044107	0.1911303
ALOX15	Model 5	G	rs2664593	major	-1.676281	0.0114152	0.138945	-3.851682	0.5483403	0.002888	0.1928984
ALOX15	Model 5	C	rs2664593	minor	8.547347	0.0288354	0.004542	2.582785	14.85871	0.002888	0.1928984
AGTR1	Model 5	A	rs6801836	major	-1.91859	0.0120892	0.1093726	-4.215252	0.4331402	0.0037741	0.1928984
AGTR1	Model 5	G	rs6801836	minor	7.013485	0.0248393	0.0064658	1.928405	12.35225	0.0037741	0.1928984
AGTR1	Model 4	A	rs389566	major	-2.010321	0.0131864	0.1238606	-4.510414	0.5552278	0.0073025	0.2109611
AGTR1	Model 4	T	rs389566	minor	5.112164	0.0198747	0.0122786	1.096373	9.287472	0.0073025	0.2109611
ALOX15	Model 4	C	rs7220870	major	-1.324662	0.0116291	0.2517796	-3.548297	0.9502382	0.0125001	0.2708355
ALOX15	Model 4	A	rs7220870	minor	7.27075	0.028819	0.0150494	1.379597	13.50424	0.0125001	0.2708355
ALOX15	Model 5	C	rs7220870	major	-1.539465	0.0115627	0.1799777	-3.745724	0.7173648	0.007965	0.2714
ALOX15	Model 5	A	rs7220870	minor	7.549802	0.0286679	0.0112725	1.673416	13.76582	0.007965	0.2714
AGTR1	Model 5	A	rs389566	major	-1.945754	0.013117	0.134448	-4.434485	0.607789	0.0127602	0.326094
AGTR1	Model 5	T	rs389566	minor	4.621645	0.0197845	0.0226035	0.6423857	8.75824	0.0127602	0.326094
ALOX15	Model 1	G	rs2664593	major	-1.631622	0.0121072	0.174531	-3.938403	0.7305533	0.0113859	0.3386382
ALOX15	Model 1	C	rs2664593	minor	7.528325	0.0305436	0.01767	1.280091	14.16203	0.0113859	0.3386382
AGTR1	Model 1	G	rs385338	major	-1.904984	0.0131032	0.1424567	-4.392159	0.6468917	0.0122286	0.3386382
AGTR1	Model 1	C	rs385338	minor	5.51253	0.0233514	0.0217728	0.7922824	10.45383	0.0122286	0.3386382
ALOX15	Model 3	G	rs2664593	major	-1.70133	0.0121356	0.1576765	-4.011818	0.6647733	0.0129645	0.4969725
ALOX15	Model 3	C	rs2664593	minor	7.297146	0.0306343	0.021704	1.044392	13.93683	0.0129645	0.4969725
ALOX15	Model 2	G	rs2664593	major	-1.665525	0.0121397	0.166816	-3.977624	0.7022458	0.0134463	0.5154415
ALOX15	Model 2	C	rs2664593	minor	7.263427	0.030585	0.0220814	1.022397	13.89002	0.0134463	0.5154415
AGTR1	Model 2	G	rs385338	major	-1.880315	0.0131456	0.1490546	-4.376071	0.6805798	0.0184429	0.5302334
AGTR1	Model 2	C	rs385338	minor	5.106848	0.0234825	0.0341649	0.3789532	10.05743	0.0184429	0.5302334
AGTR1	Model 3	G	rs385338	major	-1.879196	0.0131158	0.1483776	-4.369395	0.6758472	0.0189457	0.5446889
AGTR1	Model 3	C	rs385338	minor	5.064517	0.0234443	0.0353294	0.3463001	10.00458	0.0189457	0.5446889
AGTR1	Model 4	A	rs2638360	major	-0.6957587	0.0107405	0.5158074	-2.764364	1.416854	0.0324842	0.5630595
AGTR1	Model 4	G	rs2638360	minor	8.413332	0.0378736	0.033176	0.6571417	16.76718	0.0324842	0.5630595
VEGFA	Model 4	C	rs1109324	major	-0.4638932	0.0109374	0.6708408	-2.574939	1.692896	0.1247142	0.61467
VEGFA	Model 4	A	rs1109324	minor	5.581046	0.0349172	0.1201786	-1.402849	13.05963	0.1247142	0.61467
TLR4	Model 4	G	rs11536889	major	0.940944	0.0110589	0.3972708	-1.223412	3.152725	0.1687193	0.61467
TLR4	Model 4	C	rs11536889	minor	-4.188138	0.0341816	0.2109872	-10.39672	2.45064	0.1687193	0.61467

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
VEGFA	Model 4	T	rs1547651	major	-0.4981182	0.010978	0.6492966	-2.616175	1.666006	0.1250046	0.61467
VEGFA	Model 4	A	rs1547651	minor	5.457659	0.0343413	0.1220862	-1.40684	12.8001	0.1250046	0.61467
EDN1	Model 4	G	rs1630736	major	1.760017	0.0138113	0.206795	-0.9576377	4.552243	0.1162857	0.61467
EDN1	Model 4	A	rs1630736	minor	-2.119071	0.0179226	0.2323503	-5.497709	1.38036	0.1162857	0.61467
PTGS1	Model 4	G	rs1888943	major	-0.3568122	0.0102806	0.7281443	-2.344498	1.671331	0.0662621	0.61467
PTGS1	Model 4	A	rs1888943	minor	8.665909	0.0451186	0.0657745	-0.5308747	18.71302	0.0662621	0.61467
GRK4	Model 4	G	rs2105380	major	-0.0173472	0.0100078	0.9861727	-1.959393	1.963167	0.1605037	0.61467
GRK4	Model 4	A	rs2105380	minor	11.41277	0.0757063	0.153745	-3.950826	29.23385	0.1605037	0.61467
AGT	Model 4	G	rs2148582	major	1.39425	0.0128708	0.2822834	-1.131556	3.984584	0.1571095	0.61467
AGT	Model 4	A	rs2148582	minor	-2.250639	0.020055	0.2566258	-6.018355	1.668123	0.1571095	0.61467
VEGFA	Model 4	G	rs3025035	major	0.9468852	0.0111036	0.3962196	-1.226262	3.167844	0.1535865	0.61467
VEGFA	Model 4	A	rs3025035	minor	-3.866324	0.0306179	0.1981058	-9.465623	2.079275	0.1535865	0.61467
AGTR1	Model 4	G	rs3772616	major	1.375927	0.0128811	0.2889951	-1.151421	3.967893	0.165581	0.61467
AGTR1	Model 4	A	rs3772616	minor	-1.951173	0.0185276	0.2878	-5.447789	1.67475	0.165581	0.61467
AGT	Model 4	C	rs3789671	major	-1.407375	0.0133858	0.2899174	-3.960376	1.213493	0.0698621	0.61467
AGT	Model 4	A	rs3789671	minor	3.384666	0.0196607	0.0907591	-0.5234078	7.446274	0.0698621	0.61467
AGTR1	Model 4	G	rs385338	major	-1.147298	0.012435	0.3536496	-3.527437	1.291563	0.0589316	0.61467
AGTR1	Model 4	C	rs385338	minor	4.143869	0.0222159	0.067899	-0.2934918	8.778712	0.0589316	0.61467
PTGS2	Model 4	C	rs4648307	major	-0.4066757	0.0108014	0.7060529	-2.49294	1.724227	0.1602613	0.61467
PTGS2	Model 4	A	rs4648307	minor	5.450664	0.0374168	0.1563787	-2.005875	13.47458	0.1602613	0.61467
GRK4	Model 4	A	rs6846128	major	-0.1006154	0.0101776	0.9212304	-2.073645	1.912167	0.1702163	0.61467
GRK4	Model 4	G	rs6846128	minor	8.687417	0.0595433	0.1620997	-3.284533	22.14132	0.1702163	0.61467
AGT	Model 4	G	rs699	major	1.604084	0.0129209	0.2183833	-0.9366774	4.210011	0.1033925	0.61467
AGT	Model 4	A	rs699	minor	-2.567779	0.0198654	0.1906752	-6.288444	1.300609	0.1033925	0.61467
ALOX15	Model 4	G	rs7217186	major	-1.658083	0.0152603	0.2734992	-4.555899	1.327714	0.0992264	0.61467
ALOX15	Model 4	A	rs7217186	minor	2.528223	0.0167342	0.1360065	-0.7799851	5.946734	0.0992264	0.61467
ALOX15	Model 4	A	rs743646	major	-0.1928938	0.0102458	0.8505641	-2.177174	1.831636	0.1697855	0.61467
ALOX15	Model 4	G	rs743646	minor	7.977423	0.055144	0.1642791	-3.084263	20.30166	0.1697855	0.61467
AGT	Model 4	G	rs7549009	major	-0.8653086	0.0126776	0.493174	-3.298213	1.628804	0.1635755	0.61467
AGT	Model 4	A	rs7549009	minor	2.964803	0.0215142	0.1747591	-1.286647	7.399356	0.1635755	0.61467
ALOX15	Model 4	A	rs916055	major	1.767527	0.0132299	0.1856937	-0.8373997	4.440883	0.0821796	0.61467
ALOX15	Model 4	G	rs916055	minor	-3.005258	0.0211182	0.1488041	-6.938012	1.093693	0.0821796	0.61467
AGT	Model 4	G	rs943580	major	1.532743	0.0128445	0.2365952	-0.991417	4.121255	0.1222297	0.61467
AGT	Model 4	A	rs943580	minor	-2.473393	0.0202409	0.2162506	-6.266674	1.473397	0.1222297	0.61467
GRK4	Model 4	G	rs1024323	major	1.470019	0.0140215	0.2982338	-1.280577	4.297255	0.2035149	0.6299271
GRK4	Model 4	A	rs1024323	minor	-1.771158	0.0183273	0.3297651	-5.237004	1.821448	0.2035149	0.6299271
AGTR1	Model 4	G	rs2638363	major	-0.6042589	0.0118197	0.6082191	-2.88042	1.725248	0.1970924	0.6299271
AGTR1	Model 4	A	rs2638363	minor	3.38791	0.0258504	0.1977408	-1.719831	8.761106	0.1970924	0.6299271
AGT	Model 4	G	rs3789670	major	-0.5128763	0.0113176	0.6496875	-2.69541	1.718611	0.1922941	0.6299271
AGT	Model 4	A	rs3789670	minor	4.04215	0.0303004	0.1912523	-1.956771	10.40812	0.1922941	0.6299271
PTGS1	Model 4	G	rs3842787	major	0.5875821	0.0102557	0.5679558	-1.414128	2.629935	0.1896077	0.6299271
PTGS1	Model 4	A	rs3842787	minor	-6.555094	0.0539908	0.2095054	-15.93821	3.875384	0.1896077	0.6299271
ADRB2	Model 4	C	rs1042719	major	1.321605	0.0139575	0.3471049	-1.412603	4.131644	0.2842388	0.6606693
ADRB2	Model 4	G	rs1042719	minor	-1.505723	0.0191648	0.4287617	-5.136774	2.264312	0.2842388	0.6606693
GRK4	Model 4	C	rs1056094	major	0.8229024	0.0130034	0.5286776	-1.714223	3.42552	0.4736696	0.6606693
GRK4	Model 4	G	rs1056094	minor	-1.05692	0.0202466	0.5998383	-4.906366	2.948353	0.4736696	0.6606693

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ALOX15	Model 4	A	rs1076039	major	-0.0085023	0.0104546	0.9935125	-2.036535	2.061515	0.4768768	0.6606693
ALOX15	Model 4	T	rs1076039	minor	3.475751	0.0455103	0.4529767	-5.354458	13.1298	0.4768768	0.6606693
PTGS2	Model 4	A	rs10911905	major	-0.1205549	0.010854	0.9115304	-2.222893	2.026986	0.4256126	0.6606693
PTGS2	Model 4	C	rs10911905	minor	3.018824	0.0354817	0.4021073	-3.901972	10.43804	0.4256126	0.6606693
PTGS1	Model 4	G	rs10985620	major	0.4154915	0.0100714	0.6806536	-1.547229	2.41734	0.4060186	0.6606693
PTGS1	Model 4	C	rs10985620	minor	-4.955848	0.0645104	0.4309344	-16.24437	7.854131	0.4060186	0.6606693
ADRB2	Model 4	G	rs11168070	major	-0.3552469	0.0118407	0.7638156	-2.641109	1.984285	0.3518486	0.6606693
ADRB2	Model 4	C	rs11168070	minor	2.397434	0.024647	0.3366688	-2.431527	7.465396	0.3518486	0.6606693
PTGS1	Model 4	G	rs1213266	major	-0.1166832	0.0113435	0.9180446	-2.312877	2.128885	0.5531752	0.6606693
PTGS1	Model 4	A	rs1213266	minor	1.672077	0.0261254	0.5257515	-3.402984	7.013773	0.5531752	0.6606693
ADRB2	Model 4	G	rs12654778	major	-0.5650038	0.0131431	0.6664843	-3.093734	2.029713	0.358984	0.6606693
ADRB2	Model 4	A	rs12654778	minor	1.979754	0.021193	0.3551741	-2.169453	6.304939	0.358984	0.6606693
AGT	Model 4	A	rs1326886	major	-0.3661354	0.0122428	0.7645373	-2.728447	2.053546	0.4011588	0.6606693
AGT	Model 4	G	rs1326886	minor	2.031551	0.0231689	0.3855727	-2.4981	6.771636	0.4011588	0.6606693
VEGFA	Model 4	G	rs1413711	major	1.361541	0.0136272	0.3212488	-1.309881	4.105275	0.2454953	0.6606693
VEGFA	Model 4	A	rs1413711	minor	-1.788465	0.020235	0.3726908	-5.607295	2.184863	0.2454953	0.6606693
GRK4	Model 4	A	rs1419046	major	0.8424084	0.0130249	0.5196864	-1.699355	3.449894	0.464313	0.6606693
GRK4	Model 4	T	rs1419046	minor	-1.074776	0.0201865	0.5925583	-4.912318	2.917641	0.464313	0.6606693
EDN1	Model 4	G	rs1476046	major	-0.287444	0.0122877	0.8148269	-2.660175	2.143124	0.4643985	0.6606693
EDN1	Model 4	A	rs1476046	minor	1.93913	0.0247836	0.4385614	-2.894219	7.013055	0.4643985	0.6606693
TLR4	Model 4	A	rs1554973	major	0.7219085	0.0125812	0.5676296	-1.7314	3.236464	0.4935672	0.6606693
TLR4	Model 4	G	rs1554973	minor	-1.002425	0.0199163	0.6130672	-4.792363	2.938379	0.4935672	0.6606693
TLR4	Model 4	G	rs1927907	major	0.648302	0.0115376	0.5755454	-1.602154	2.950229	0.4673826	0.6606693
TLR4	Model 4	A	rs1927907	minor	-1.697193	0.0280909	0.5424218	-6.963176	3.86685	0.4673826	0.6606693
TLR4	Model 4	A	rs1927914	major	-0.4163983	0.0149104	0.7796505	-3.284501	2.536758	0.5593389	0.6606693
TLR4	Model 4	G	rs1927914	minor	1.017022	0.0164752	0.5392317	-2.192791	4.332173	0.5593389	0.6606693
TLR4	Model 4	C	rs2149356	major	-0.4259498	0.0147335	0.7720897	-3.260234	2.491373	0.5511984	0.6606693
TLR4	Model 4	A	rs2149356	minor	1.043123	0.0167414	0.5354958	-2.218546	4.41359	0.5511984	0.6606693
GRK4	Model 4	A	rs2185886	major	0.9746792	0.0144009	0.5007581	-1.835504	3.86531	0.4362743	0.6606693
GRK4	Model 4	G	rs2185886	minor	-0.9527674	0.0172531	0.5791031	-4.246099	2.453834	0.4362743	0.6606693
PTGS2	Model 4	G	rs2206593	major	0.404961	0.0101047	0.6892754	-1.563987	2.413292	0.4915429	0.6606693
PTGS2	Model 4	A	rs2206593	minor	-4.444533	0.0701559	0.5171133	-16.72039	9.640846	0.4915429	0.6606693
GRK4	Model 4	G	rs2471327	major	1.210194	0.014172	0.3961928	-1.562401	4.060881	0.313402	0.6606693
GRK4	Model 4	A	rs2471327	minor	-1.347493	0.0180258	0.4518571	-4.77203	2.200194	0.313402	0.6606693
GRK4	Model 4	A	rs2471337	major	0.7096036	0.0128874	0.5833533	-1.802354	3.285819	0.5322576	0.6606693
GRK4	Model 4	G	rs2471337	minor	-0.9598214	0.0208399	0.6436133	-4.92366	3.169274	0.5322576	0.6606693
GRK4	Model 4	A	rs2471347	major	0.7898748	0.0137849	0.5682977	-1.896794	3.550121	0.5537509	0.6606693
GRK4	Model 4	G	rs2471347	minor	-0.7899256	0.0196144	0.6860601	-4.531538	3.098329	0.5537509	0.6606693
GRK4	Model 4	A	rs2488806	major	0.9895816	0.0142279	0.4890331	-1.787724	3.845425	0.4178487	0.6606693
GRK4	Model 4	C	rs2488806	minor	-1.069751	0.0179959	0.550213	-4.498327	2.481914	0.4178487	0.6606693
GRK4	Model 4	A	rs2488813	major	1.054868	0.0121915	0.3895995	-1.3312	3.498638	0.2546132	0.6606693
GRK4	Model 4	T	rs2488813	minor	-2.254038	0.0240712	0.3438075	-6.758473	2.468003	0.2546132	0.6606693
GRK4	Model 4	G	rs2488815	major	1.27015	0.0141096	0.371254	-1.492047	4.109799	0.2710139	0.6606693
GRK4	Model 4	A	rs2488815	minor	-1.521357	0.0180975	0.3971399	-4.953215	2.034416	0.2710139	0.6606693
AGTR1	Model 4	A	rs275645	major	-1.080599	0.0155473	0.4848247	-4.049415	1.980075	0.2649879	0.6606693
AGTR1	Model 4	G	rs275645	minor	1.724466	0.0162914	0.2942066	-1.472341	5.024996	0.2649879	0.6606693

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 4	G	rs275646	major	0.5189248	0.0104781	0.6214373	-1.524342	2.604587	0.4983279	0.6606693
AGTR1	Model 4	A	rs275646	minor	-2.754861	0.0462381	0.5458748	-11.18016	6.469652	0.4983279	0.6606693
GRK4	Model 4	A	rs2960298	major	0.7381167	0.0128614	0.5675918	-1.769544	3.309794	0.5132122	0.6606693
GRK4	Model 4	G	rs2960298	minor	-1.007767	0.0208533	0.6272744	-4.972178	3.122033	0.5132122	0.6606693
GRK4	Model 4	C	rs2960306	major	0.7669354	0.0129881	0.5565052	-1.765832	3.365005	0.5251137	0.6606693
GRK4	Model 4	A	rs2960306	minor	-0.9045123	0.0203106	0.6547083	-4.771831	3.119862	0.5251137	0.6606693
GRK4	Model 4	G	rs3021140	major	0.8373563	0.012843	0.5163075	-1.669226	3.407835	0.4351724	0.6606693
GRK4	Model 4	A	rs3021140	minor	-1.235533	0.020767	0.5495382	-5.174789	2.867369	0.4351724	0.6606693
VEGFA	Model 4	A	rs3025010	major	0.870111	0.0136821	0.5267498	-1.798918	3.611682	0.5231842	0.6606693
VEGFA	Model 4	G	rs3025010	minor	-0.9004205	0.0206483	0.6614453	-4.830909	3.192398	0.5231842	0.6606693
VEGFA	Model 4	A	rs3025033	major	0.8704729	0.0115078	0.4515395	-1.379182	3.171445	0.307054	0.6606693
VEGFA	Model 4	G	rs3025033	minor	-2.407637	0.0280782	0.3856206	-7.63325	3.113613	0.307054	0.6606693
EDN1	Model 4	A	rs3087459	major	-0.1060472	0.0117561	0.9281033	-2.381436	2.222378	0.5641099	0.6606693
EDN1	Model 4	C	rs3087459	minor	1.72279	0.0268106	0.5242018	-3.484499	7.211027	0.5641099	0.6606693
AGTR1	Model 4	A	rs422858	major	-0.1726924	0.011511	0.8806743	-2.399703	2.105133	0.4666126	0.6606693
AGTR1	Model 4	C	rs422858	minor	2.33535	0.0297063	0.4372793	-3.452806	8.470515	0.4666126	0.6606693
ACE	Model 4	A	rs4351	major	-0.5345188	0.0152773	0.7258002	-3.46866	2.488808	0.5065709	0.6606693
ACE	Model 4	G	rs4351	minor	1.204801	0.0174067	0.4916068	-2.189728	4.717137	0.5065709	0.6606693
ACE	Model 4	G	rs4362	major	-0.4421572	0.0148984	0.7661933	-3.307251	2.507832	0.5557343	0.6606693
ACE	Model 4	A	rs4362	minor	1.067626	0.0173571	0.5407863	-2.312793	4.565023	0.5557343	0.6606693
AGTR1	Model 4	G	rs4488792	major	0.9746011	0.0124805	0.4372718	-1.4654	3.475024	0.3149729	0.6606693
AGTR1	Model 4	A	rs4488792	minor	-1.588209	0.0203879	0.4324948	-5.443168	2.423912	0.3149729	0.6606693
TLR4	Model 4	G	rs4986791	major	0.0842147	0.0100445	0.9332276	-1.86687	2.074091	0.5251057	0.6606693
TLR4	Model 4	A	rs4986791	minor	4.949282	0.0731688	0.5092692	-9.071905	21.13255	0.5251057	0.6606693
EDN1	Model 4	C	rs5370	major	-0.3796394	0.0121172	0.7536599	-2.717669	2.014581	0.3747381	0.6606693
EDN1	Model 4	A	rs5370	minor	2.383383	0.0256312	0.3583351	-2.632921	7.658124	0.3747381	0.6606693
PTGS1	Model 4	C	rs5788	major	0.6589156	0.0117686	0.5769327	-1.636323	3.007711	0.5218729	0.6606693
PTGS1	Model 4	A	rs5788	minor	-1.075055	0.0228322	0.6360312	-5.404379	3.452407	0.5218729	0.6606693
ALOX15	Model 4	G	rs6502804	major	1.77759	0.0159124	0.2684336	-1.347642	5.001826	0.2286623	0.6606693
ALOX15	Model 4	A	rs6502804	minor	-1.336628	0.0164804	0.4144035	-4.472633	1.902326	0.2286623	0.6606693
VEGFA	Model 4	A	rs699946	major	1.208712	0.0124718	0.3356073	-1.235268	3.713169	0.2325898	0.6606693
VEGFA	Model 4	G	rs699946	minor	-2.260149	0.0236277	0.3335061	-6.683213	2.372561	0.2325898	0.6606693
VEGFA	Model 4	C	rs699947	major	0.9107341	0.0134569	0.5006486	-1.715999	3.607669	0.4895426	0.6606693
VEGFA	Model 4	A	rs699947	minor	-0.9618948	0.0203862	0.6355186	-4.841075	3.075422	0.4895426	0.6606693
ALOX15	Model 4	A	rs748694	major	1.424656	0.0156131	0.3651345	-1.632037	4.576333	0.3156883	0.6606693
ALOX15	Model 4	G	rs748694	minor	-1.090716	0.016169	0.4977521	-4.176066	2.093977	0.3156883	0.6606693
TLR4	Model 4	C	rs7873784	major	0.7107612	0.0110868	0.5230849	-1.454042	2.92312	0.3501039	0.6606693
TLR4	Model 4	G	rs7873784	minor	-2.659845	0.0327422	0.4105004	-8.71029	3.791607	0.3501039	0.6606693
VEGFA	Model 4	C	rs833060	major	0.8019812	0.0128868	0.5354998	-1.712149	3.38042	0.5275731	0.6606693
VEGFA	Model 4	A	rs833060	minor	-0.984679	0.0222379	0.6564248	-5.207607	3.426378	0.5275731	0.6606693
PTGS1	Model 4	G	rs876567	major	0.4003582	0.0099766	0.6888765	-1.543775	2.382881	0.3450608	0.6606693
PTGS1	Model 4	A	rs876567	minor	-6.707618	0.0763769	0.363534	-19.67808	8.357327	0.3450608	0.6606693
PTGS1	Model 4	G	rs2282169	major	0.6918693	0.0121343	0.5700167	-1.674604	3.115298	0.5728236	0.6619295
PTGS1	Model 4	C	rs2282169	minor	-0.8563544	0.022557	0.70308	-5.144099	3.625208	0.5728236	0.6619295
PTGS1	Model 4	A	rs1330344	major	0.6554171	0.0132991	0.6233787	-1.934343	3.313569	0.6143638	0.6655608
PTGS1	Model 4	G	rs1330344	minor	-0.6647019	0.0197846	0.7361193	-4.44291	3.262892	0.6143638	0.6655608

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ALOX15	Model 4	A	rs1871346	major	0.3543133	0.0101455	0.7274522	-1.621504	2.369813	0.6128576	0.6655608
ALOX15	Model 4	G	rs1871346	minor	-2.487851	0.0549899	0.6469495	-12.45098	8.60909	0.6128576	0.6655608
AGTR1	Model 4	G	rs2131127	major	-0.3025078	0.0147929	0.8377657	-3.151583	2.630382	0.6024951	0.6655608
AGTR1	Model 4	A	rs2131127	minor	1.033037	0.0174933	0.5569981	-2.372292	4.557147	0.6024951	0.6655608
ACE	Model 4	G	rs4353	major	-0.4163584	0.0158217	0.7920612	-3.457057	2.720109	0.6067713	0.6655608
ACE	Model 4	A	rs4353	minor	0.8976373	0.0163298	0.5843372	-2.280552	4.179193	0.6067713	0.6655608
ACE	Model 4	G	rs4359	major	-0.4061518	0.0150342	0.786676	-3.298015	2.572192	0.5862304	0.6655608
ACE	Model 4	A	rs4359	minor	0.9901269	0.0172401	0.5677966	-2.365326	4.460898	0.5862304	0.6655608
PTGS1	Model 4	G	rs10306202	major	0.4854499	0.0111773	0.6649146	-1.691958	2.711085	0.6252242	0.6689642
PTGS1	Model 4	A	rs10306202	minor	-1.112452	0.0291417	0.7011506	-6.602309	4.700095	0.6252242	0.6689642
AGTR1	Model 4	A	rs2320019	major	0.1105958	0.0107341	0.9180035	-1.97358	2.239084	0.6625705	0.674762
AGTR1	Model 4	G	rs2320019	minor	1.711613	0.0334481	0.6119917	-4.742434	8.602945	0.6625705	0.674762
GRK4	Model 4	A	rs2857844	major	-0.1899036	0.0153448	0.9014388	-3.14702	2.857499	0.7007144	0.674762
GRK4	Model 4	G	rs2857844	minor	0.7491525	0.0159404	0.63973	-2.349851	3.946505	0.7007144	0.674762
AGTR1	Model 4	A	rs409742	major	0.0246579	0.0115666	0.9829981	-2.217395	2.318118	0.6994951	0.674762
AGTR1	Model 4	G	rs409742	minor	1.322241	0.028958	0.6502054	-4.268318	7.239278	0.6994951	0.674762
ACE	Model 4	G	rs4277404	major	0.1458846	0.0100389	0.8845721	-1.805322	2.135863	0.6886142	0.674762
ACE	Model 4	A	rs4277404	minor	3.478621	0.0801321	0.6696673	-11.56135	21.07631	0.6886142	0.674762
ACE	Model 4	G	rs4309	major	-0.2364505	0.0153489	0.8774574	-3.192974	2.810366	0.6914776	0.674762
ACE	Model 4	A	rs4309	minor	0.7767521	0.0168252	0.6457053	-2.492343	4.155449	0.6914776	0.674762
ACE	Model 4	A	rs4316	major	-0.2315675	0.0158615	0.8838221	-3.285442	2.918737	0.6984775	0.674762
ACE	Model 4	G	rs4316	minor	0.7813323	0.0167803	0.6428809	-2.479323	4.15101	0.6984775	0.674762
AGTR1	Model 4	G	rs4681443	major	-0.0797567	0.0118741	0.9464396	-2.378331	2.272939	0.670633	0.674762
AGTR1	Model 4	A	rs4681443	minor	1.035715	0.0217867	0.6363571	-3.187811	5.443496	0.670633	0.674762
ACE	Model 4	A	rs8066276	major	0.7127921	0.0147237	0.6296319	-2.152034	3.661495	0.6657174	0.674762
ACE	Model 4	G	rs8066276	minor	-0.4183321	0.0180503	0.8163959	-3.879733	3.167718	0.6657174	0.674762
ALOX15	Model 4	G	rs9894225	major	0.5332685	0.0118299	0.6531092	-1.770898	2.891484	0.6539869	0.674762
ALOX15	Model 4	A	rs9894225	minor	-0.7131715	0.0233787	0.7595586	-5.159983	3.94214	0.6539869	0.674762
TLR4	Model 4	G	rs1927911	major	-0.1321851	0.0138852	0.9241261	-2.813384	2.622983	0.7135827	0.6796026
TLR4	Model 4	A	rs1927911	minor	0.8164698	0.0186994	0.6637605	-2.811571	4.579946	0.7135827	0.6796026
AGTR1	Model 5	A	rs2638360	major	-0.8110567	0.0106914	0.4464178	-2.867905	1.289347	0.0334403	0.6836684
AGTR1	Model 5	G	rs2638360	minor	8.198157	0.0377015	0.0368754	0.4912512	16.49612	0.0334403	0.6836684
ADRB2	Model 4	G	rs1042713	major	0.645999	0.0152581	0.6731014	-2.319287	3.701302	0.7340054	0.6840194
ADRB2	Model 4	A	rs1042713	minor	-0.2187985	0.0168434	0.8965577	-3.459036	3.130192	0.7340054	0.6840194
VEGFB	Model 4	G	rs5949442	major	-0.0478524	0.013462	0.9716445	-2.650597	2.624479	0.7288997	0.6840194
VEGFB	Model 4	A	rs5949442	minor	0.896854	0.0204186	0.6620071	-3.061288	5.016612	0.7288997	0.6840194
GRK4	Model 4	A	rs2798298	major	0.546582	0.0141462	0.7000753	-2.202878	3.37334	0.7486661	0.6902595
GRK4	Model 4	G	rs2798298	minor	-0.3003181	0.018938	0.8738442	-3.93312	3.469851	0.7486661	0.6902595
PTGS1	Model 4	G	rs883484	major	0.4317499	0.0124167	0.7286874	-1.982879	2.905863	0.7590444	0.6924616
PTGS1	Model 4	A	rs883484	minor	-0.4368581	0.022908	0.8484715	-4.808263	4.135291	0.7590444	0.6924616
GRK4	Model 4	C	rs1008210	major	0.4710086	0.0140294	0.7377399	-2.254021	3.272008	0.8091517	0.7012648
GRK4	Model 4	A	rs1008210	minor	-0.1726175	0.0192589	0.9285378	-3.870552	3.66757	0.8091517	0.7012648
ACE	Model 4	C	rs4303	major	0.1648056	0.009969	0.8688346	-1.773313	2.141165	0.8069492	0.7012648
ACE	Model 4	A	rs4303	minor	2.363424	0.0876051	0.7898002	-13.78652	21.53865	0.8069492	0.7012648
ACE	Model 4	A	rs4363	major	-0.0792174	0.0149538	0.957746	-2.965294	2.892699	0.7855547	0.7012648
ACE	Model 4	G	rs4363	minor	0.6177093	0.0173013	0.7219672	-2.737038	4.088167	0.7855547	0.7012648

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
VEGFA	Model 4	G	rs735286	major	0.4268695	0.0128893	0.7411118	-2.078395	2.99623	0.8082904	0.7012648
VEGFA	Model 4	A	rs735286	minor	-0.2601088	0.0222279	0.9067482	-4.512065	4.181181	0.8082904	0.7012648
AGT	Model 4	A	rs7536290	major	0.4307413	0.0123256	0.7273751	-1.966373	2.88647	0.7820216	0.7012648
AGT	Model 4	G	rs7536290	minor	-0.3817771	0.0239743	0.8732685	-4.954438	4.410875	0.7820216	0.7012648
ACE	Model 4	T	rs4291	major	0.027886	0.0134202	0.9834284	-2.568865	2.693846	0.8289755	0.7113321
ACE	Model 4	A	rs4291	minor	0.6154173	0.0204488	0.7642148	-3.337402	4.729879	0.8289755	0.7113321
VEGFA	Model 4	A	rs833069	major	0.386026	0.014894	0.7959334	-2.50206	3.359663	0.8395627	0.7133539
VEGFA	Model 4	G	rs833069	minor	-0.1344123	0.01751	0.9387864	-3.503561	3.352369	0.8395627	0.7133539
PTGS1	Model 4	A	rs4836885	major	0.3774921	0.0116799	0.7470731	-1.894261	2.70185	0.8609725	0.7244429
PTGS1	Model 4	G	rs4836885	minor	-0.1095937	0.0235537	0.9628773	-4.616145	4.609877	0.8609725	0.7244429
AGT	Model 4	G	rs2478545	major	0.1189481	0.0129586	0.9269258	-2.391884	2.694368	0.8830183	0.7297181
AGT	Model 4	A	rs2478545	minor	0.5096174	0.0204696	0.8039297	-3.44298	4.624016	0.8830183	0.7297181
AGTR1	Model 4	G	rs718858	major	0.2039635	0.0110621	0.8538992	-1.945199	2.400231	0.8840816	0.7297181
AGTR1	Model 4	A	rs718858	minor	0.7341836	0.0325999	0.8225015	-5.500871	7.380627	0.8840816	0.7297181
GRK4	Model 5	G	rs1024323	major	1.367558	0.0139458	0.330302	-1.365618	4.176471	0.1942759	0.7360982
GRK4	Model 5	A	rs1024323	minor	-1.921777	0.0182459	0.2878045	-5.367206	1.649095	0.1942759	0.7360982
ADRB2	Model 5	C	rs1042719	major	1.45026	0.0138779	0.2997557	-1.272022	4.247604	0.1854964	0.7360982
ADRB2	Model 5	G	rs1042719	minor	-2.021598	0.0190719	0.2845038	-5.616451	1.710174	0.1854964	0.7360982
VEGFA	Model 5	C	rs1109324	major	-0.5497885	0.0108752	0.6123098	-2.647135	1.592742	0.1454997	0.7360982
VEGFA	Model 5	A	rs1109324	minor	5.131934	0.0347104	0.149669	-1.782446	12.53308	0.1454997	0.7360982
ADRB2	Model 5	G	rs11168070	major	-0.5369283	0.0117723	0.6475384	-2.805597	1.784695	0.3076521	0.7360982
ADRB2	Model 5	C	rs11168070	minor	2.460184	0.0245045	0.3215256	-2.344471	7.501228	0.3076521	0.7360982
TLR4	Model 5	G	rs11536889	major	0.6830644	0.0110075	0.536429	-1.465833	2.878826	0.2619881	0.7360982
TLR4	Model 5	C	rs11536889	minor	-3.486447	0.034002	0.2968931	-9.70874	3.164646	0.2619881	0.7360982
ADRB2	Model 5	G	rs12654778	major	-0.8453533	0.0130702	0.5161455	-3.353146	1.727512	0.2718901	0.7360982
ADRB2	Model 5	A	rs12654778	minor	2.1843	0.0210679	0.3053141	-1.949193	6.492047	0.2718901	0.7360982
VEGFA	Model 5	G	rs1413711	major	1.122881	0.0135765	0.4110075	-1.532452	3.849818	0.2999741	0.7360982
VEGFA	Model 5	A	rs1413711	minor	-1.675012	0.0201255	0.4014832	-5.477961	2.280943	0.2999741	0.7360982
VEGFA	Model 5	T	rs1547651	major	-0.6311278	0.010914	0.5619753	-2.734165	1.51738	0.1194683	0.7360982
VEGFA	Model 5	A	rs1547651	minor	5.368253	0.0341234	0.1257375	-1.448359	12.65635	0.1194683	0.7360982
EDN1	Model 5	G	rs1630736	major	1.503907	0.0137406	0.2775884	-1.193231	4.274669	0.1471545	0.7360982
EDN1	Model 5	A	rs1630736	minor	-2.055439	0.0178277	0.2443139	-5.418688	1.427404	0.1471545	0.7360982
PTGS1	Model 5	G	rs1888943	major	-0.4554493	0.0102226	0.6552979	-2.430073	1.559136	0.0779452	0.7360982
PTGS1	Model 5	A	rs1888943	minor	8.129769	0.0448595	0.0817525	-0.9713537	18.06732	0.0779452	0.7360982
GRK4	Model 5	G	rs2105380	major	-0.1406293	0.0099482	0.887534	-2.068835	1.825541	0.171391	0.7360982
GRK4	Model 5	A	rs2105380	minor	10.9095	0.0753339	0.1696041	-4.314887	28.55622	0.171391	0.7360982
AGT	Model 5	G	rs2148582	major	0.9453238	0.0128445	0.4640258	-1.564238	3.518866	0.3031845	0.7360982
AGT	Model 5	A	rs2148582	minor	-1.703181	0.0199713	0.3899077	-5.476489	2.220754	0.3031845	0.7360982
PTGS2	Model 5	G	rs2206593	major	0.3693082	0.0100517	0.7138956	-1.588705	2.366279	0.2949839	0.7360982
PTGS2	Model 5	A	rs2206593	minor	-6.900779	0.0699734	0.3070858	-18.83205	6.784327	0.2949839	0.7360982
GRK4	Model 5	G	rs2471327	major	1.303197	0.0140991	0.3586637	-1.457871	4.141628	0.2233219	0.7360982
GRK4	Model 5	A	rs2471327	minor	-1.771387	0.0179659	0.3200704	-5.170073	1.749108	0.2233219	0.7360982
GRK4	Model 5	A	rs2488806	major	1.082193	0.0141542	0.4471567	-1.683468	3.925653	0.3096413	0.7360982
GRK4	Model 5	C	rs2488806	minor	-1.487424	0.0179336	0.4035603	-4.889921	2.036795	0.3096413	0.7360982
GRK4	Model 5	A	rs2488813	major	0.9725319	0.0121256	0.4249612	-1.398871	3.400968	0.2312041	0.7360982
GRK4	Model 5	T	rs2488813	minor	-2.481235	0.0239406	0.294208	-6.951383	2.203664	0.2312041	0.7360982

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
GRK4	Model 5	G	rs2488815	major	1.296616	0.0140347	0.3588798	-1.451829	4.121713	0.2131428	0.7360982
GRK4	Model 5	A	rs2488815	minor	-1.842692	0.0180208	0.302287	-5.249106	1.686187	0.2131428	0.7360982
AGTR1	Model 5	G	rs2638363	major	-0.5798861	0.0117594	0.621018	-2.84511	1.738153	0.2842084	0.7360982
AGTR1	Model 5	A	rs2638363	minor	2.707492	0.0257181	0.2991689	-2.341321	8.017321	0.2842084	0.7360982
VEGFA	Model 5	A	rs3025033	major	0.7577197	0.0114435	0.5096344	-1.477003	3.043131	0.2966051	0.7360982
VEGFA	Model 5	G	rs3025033	minor	-2.574046	0.0279685	0.3513613	-7.770933	2.915674	0.2966051	0.7360982
VEGFA	Model 5	G	rs3025035	major	0.8604653	0.0110503	0.4383179	-1.300508	3.068752	0.1347632	0.7360982
VEGFA	Model 5	A	rs3025035	minor	-4.152449	0.0304608	0.164135	-9.707281	1.744118	0.1347632	0.7360982
AGTR1	Model 5	G	rs3772616	major	1.368125	0.0127949	0.2884819	-1.142332	3.942334	0.1245198	0.7360982
AGTR1	Model 5	A	rs3772616	minor	-2.288039	0.0184213	0.2092321	-5.753012	1.304322	0.1245198	0.7360982
AGT	Model 5	G	rs3789670	major	-0.469204	0.0112573	0.6761985	-2.6412	1.751247	0.3088809	0.7360982
AGT	Model 5	A	rs3789670	minor	3.060862	0.0302346	0.3189153	-2.868953	9.35269	0.3088809	0.7360982
AGT	Model 5	C	rs3789671	major	-1.215329	0.0133194	0.3588194	-3.760785	1.397452	0.1403658	0.7360982
AGT	Model 5	A	rs3789671	minor	2.662987	0.0196237	0.1807861	-1.210631	6.688493	0.1403658	0.7360982
PTGS1	Model 5	G	rs3842787	major	0.5039496	0.0101974	0.6221548	-1.484839	2.532887	0.1400611	0.7360982
PTGS1	Model 5	A	rs3842787	minor	-7.454068	0.0537428	0.1497842	-16.70645	2.826081	0.1400611	0.7360982
AGTR1	Model 5	G	rs385338	major	-1.158699	0.0123715	0.3463926	-3.526552	1.26727	0.0803871	0.7360982
AGTR1	Model 5	C	rs385338	minor	3.707004	0.0221136	0.1000738	-0.6918308	8.300685	0.0803871	0.7360982
AGTR1	Model 5	G	rs4488792	major	0.9303468	0.0124022	0.4554343	-1.49348	3.413814	0.2637815	0.7360982
AGTR1	Model 5	A	rs4488792	minor	-1.896751	0.0202658	0.3449252	-5.717064	2.078359	0.2637815	0.7360982
PTGS2	Model 5	C	rs4648307	major	-0.5744864	0.0107461	0.5919813	-2.64669	1.541825	0.1322222	0.7360982
PTGS2	Model 5	A	rs4648307	minor	5.672005	0.0372003	0.1383779	-1.758505	13.66452	0.1322222	0.7360982
ALOX15	Model 5	G	rs6502804	major	1.843875	0.0158291	0.2486733	-1.267275	5.053061	0.1715085	0.7360982
ALOX15	Model 5	A	rs6502804	minor	-1.678054	0.0164304	0.3032697	-4.793871	1.539734	0.1715085	0.7360982
GRK4	Model 5	A	rs6846128	major	-0.196742	0.0101226	0.8457844	-2.157319	1.803121	0.2108056	0.7360982
GRK4	Model 5	G	rs6846128	minor	7.77107	0.0594572	0.208431	-4.083753	21.0911	0.2108056	0.7360982
AGT	Model 5	G	rs699	major	1.099266	0.0129027	0.3970206	-1.425353	3.688543	0.2366669	0.7360982
AGT	Model 5	A	rs699	minor	-1.93228	0.019806	0.3247891	-5.666239	1.949479	0.2366669	0.7360982
VEGFA	Model 5	A	rs699946	major	1.06053	0.0124042	0.3952646	-1.366801	3.547596	0.2391268	0.7360982
VEGFA	Model 5	G	rs699946	minor	-2.337758	0.0234944	0.3142552	-6.732961	2.264569	0.2391268	0.7360982
ALOX15	Model 5	G	rs7217186	major	-2.082399	0.015239	0.1676112	-4.963739	0.8862984	0.0562899	0.7360982
ALOX15	Model 5	A	rs7217186	minor	2.757131	0.0166685	0.1030582	-0.5456737	6.169619	0.0562899	0.7360982
ALOX15	Model 5	A	rs743646	major	-0.315835	0.0101901	0.7562957	-2.286996	1.69509	0.1806996	0.7360982
ALOX15	Model 5	G	rs743646	minor	7.594629	0.0548784	0.1825514	-3.377554	19.81278	0.1806996	0.7360982
ALOX15	Model 5	A	rs748694	major	1.588349	0.0155412	0.3108319	-1.459399	4.730361	0.213327	0.7360982
ALOX15	Model 5	G	rs748694	minor	-1.521746	0.0161311	0.3420305	-4.586563	1.641518	0.213327	0.7360982
AGT	Model 5	G	rs7549009	major	-0.9354599	0.0126128	0.4563473	-3.354378	1.544001	0.1846487	0.7360982
AGT	Model 5	A	rs7549009	minor	2.692379	0.0214351	0.21547	-1.53256	7.098597	0.1846487	0.7360982
TLR4	Model 5	C	rs7873784	major	0.7040045	0.0110529	0.5257633	-1.454113	2.909384	0.24734	0.7360982
TLR4	Model 5	G	rs7873784	minor	-3.450797	0.0326798	0.2828169	-9.440997	2.935637	0.24734	0.7360982
ALOX15	Model 5	A	rs916055	major	1.575784	0.0131582	0.2350262	-1.010329	4.229458	0.0915035	0.7360982
ALOX15	Model 5	G	rs916055	minor	-3.033082	0.0210265	0.1432813	-6.947978	1.046523	0.0915035	0.7360982
AGT	Model 5	G	rs943580	major	1.02601	0.0128206	0.4261039	-1.480941	3.596754	0.2750491	0.7360982
AGT	Model 5	A	rs943580	minor	-1.80276	0.020178	0.3674989	-5.610498	2.158585	0.2750491	0.7360982
PTGS1	Model 5	G	rs10985620	major	0.3228159	0.010012	0.7475892	-1.62665	2.310915	0.3255952	0.740329
PTGS1	Model 5	C	rs10985620	minor	-5.972348	0.0642781	0.3382722	-17.10239	6.652044	0.3255952	0.740329

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 5	A	rs275645	major	-1.037267	0.0154565	0.5000923	-3.990315	2.006611	0.3259057	0.740329
AGTR1	Model 5	G	rs275645	minor	1.419024	0.0162136	0.3850271	-1.753211	4.693685	0.3259057	0.740329
GRK4	Model 4	G	rs1801058	major	0.3110315	0.0139144	0.8234372	-2.387659	3.084332	0.9292614	0.740407
GRK4	Model 4	A	rs1801058	minor	0.0748445	0.0193503	0.9691657	-3.649505	3.943156	0.9292614	0.740407
TLR4	Model 4	A	rs1927906	major	0.2259055	0.0110677	0.8384865	-1.924804	2.423778	0.9559998	0.740407
TLR4	Model 4	G	rs1927906	minor	0.0493684	0.0285614	0.9862161	-5.397458	5.8098	0.9559998	0.740407
ALOX15	Model 4	A	rs2255888	major	0.2691012	0.0121152	0.8244997	-2.083784	2.678525	0.953453	0.740407
ALOX15	Model 4	G	rs2255888	minor	0.113201	0.0218814	0.9587744	-4.089564	4.50013	0.953453	0.740407
TLR4	Model 4	A	rs2737191	major	0.2779184	0.0110575	0.8018729	-1.871953	2.47489	0.9712544	0.740407
TLR4	Model 4	G	rs2737191	minor	0.1552588	0.0304702	0.9594036	-5.650961	6.318792	0.9712544	0.740407
ACE	Model 4	G	rs4295	major	0.1963029	0.0136466	0.885761	-2.448103	2.912392	0.9612843	0.740407
ACE	Model 4	C	rs4295	minor	0.3282301	0.0201603	0.8709107	-3.558783	4.371907	0.9612843	0.740407
ACE	Model 4	G	rs4305	major	0.1723216	0.0156787	0.9125794	-2.859126	3.298371	0.976975	0.740407
ACE	Model 4	A	rs4305	minor	0.2447555	0.0161478	0.8797013	-2.878223	3.468154	0.976975	0.740407
ACE	Model 4	G	rs4311	major	0.1752332	0.0138253	0.8992532	-2.502781	2.926806	0.9565557	0.740407
ACE	Model 4	A	rs4311	minor	0.3235791	0.0199865	0.8716238	-3.530393	4.331518	0.9565557	0.740407
ACE	Model 4	A	rs4459610	major	0.3018404	0.0151147	0.841991	-2.625943	3.317655	0.9681579	0.740407
ACE	Model 4	T	rs4459610	minor	0.1994985	0.01715	0.9075098	-3.112571	3.62479	0.9681579	0.740407
ACE	Model 4	G	rs4461142	major	0.2490081	0.0136557	0.855525	-2.398535	2.968369	0.9824632	0.740407
ACE	Model 4	A	rs4461142	minor	0.1906424	0.0196133	0.9226603	-3.587742	4.117101	0.9824632	0.740407
ACE	Model 4	A	rs4968591	major	0.2583712	0.0123989	0.835183	-2.148685	2.724638	0.9691585	0.740407
ACE	Model 4	G	rs4968591	minor	0.1468814	0.0233462	0.9498841	-4.332358	4.835843	0.9691585	0.740407
TLR4	Model 5	A	rs1554973	major	0.783411	0.012525	0.5333997	-1.660551	3.288111	0.3647364	0.7948409
TLR4	Model 5	G	rs1554973	minor	-1.488149	0.0198439	0.4500901	-5.246058	2.418797	0.3647364	0.7948409
GRK4	Model 5	A	rs2185886	major	0.9884666	0.0143248	0.4924626	-1.807462	3.864007	0.365454	0.7948409
GRK4	Model 5	G	rs2185886	minor	-1.240374	0.0171846	0.4678193	-4.511314	2.142611	0.365454	0.7948409
PTGS2	Model 5	A	rs10911905	major	-0.2823301	0.010802	0.7935778	-2.371318	1.851356	0.3748859	0.7965437
PTGS2	Model 5	C	rs10911905	minor	3.199807	0.0353245	0.3727996	-3.70347	10.59797	0.3748859	0.7965437
GRK4	Model 5	G	rs3021140	major	0.7954328	0.012774	0.5352471	-1.696819	3.35087	0.3818215	0.7965437
GRK4	Model 5	A	rs3021140	minor	-1.512001	0.02066	0.4610283	-5.420389	2.557897	0.3818215	0.7965437
GRK4	Model 5	C	rs1056094	major	0.7471586	0.01293	0.5649465	-1.773925	3.332948	0.4391607	0.799368
GRK4	Model 5	G	rs1056094	minor	-1.2691	0.0201456	0.5262301	-5.091503	2.70725	0.4391607	0.799368
ALOX15	Model 5	A	rs1076039	major	-0.1280812	0.0103978	0.9019263	-2.142809	1.928126	0.4810838	0.799368
ALOX15	Model 5	T	rs1076039	minor	3.304006	0.0453225	0.4734099	-5.476772	12.90048	0.4810838	0.799368
AGT	Model 5	A	rs1326886	major	-0.4695639	0.0121702	0.6990313	-2.815586	1.933091	0.4191141	0.799368
AGT	Model 5	G	rs1326886	minor	1.825382	0.0230887	0.4335391	-2.679816	6.539136	0.4191141	0.799368
GRK4	Model 5	A	rs1419046	major	0.778513	0.0129524	0.5494879	-1.747665	3.369642	0.4222611	0.799368
GRK4	Model 5	T	rs1419046	minor	-1.310305	0.0200873	0.5115786	-5.120262	2.652642	0.4222611	0.799368
ALOX15	Model 5	A	rs1871346	major	0.2612751	0.0100852	0.7958971	-1.701095	2.262821	0.5336512	0.799368
ALOX15	Model 5	G	rs1871346	minor	-3.202606	0.0547111	0.5520149	-13.04521	7.754109	0.5336512	0.799368
TLR4	Model 5	G	rs1927907	major	0.5182054	0.0114721	0.6524181	-1.716725	2.803957	0.4726248	0.799368
TLR4	Model 5	A	rs1927907	minor	-1.785264	0.0279505	0.5194035	-7.020939	3.745234	0.4726248	0.799368
GRK4	Model 5	A	rs2471337	major	0.6931105	0.0128174	0.5900812	-1.804954	3.254725	0.4554617	0.799368
GRK4	Model 5	G	rs2471337	minor	-1.288301	0.0207355	0.5318912	-5.219596	2.806056	0.4554617	0.799368
AGTR1	Model 5	G	rs275646	major	0.3806308	0.0104216	0.7155337	-1.648949	2.452093	0.520282	0.799368
AGTR1	Model 5	A	rs275646	minor	-2.717519	0.0461041	0.5502509	-11.12273	6.482579	0.520282	0.799368

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
GRK4	Model 5	A	rs2960298	major	0.7093509	0.0127928	0.5807044	-1.784375	3.266394	0.4456078	0.799368
GRK4	Model 5	G	rs2960298	minor	-1.313803	0.0207486	0.5240131	-5.246527	2.782147	0.4456078	0.799368
GRK4	Model 5	C	rs2960306	major	0.7480328	0.012923	0.5642818	-1.771722	3.332425	0.450023	0.799368
GRK4	Model 5	A	rs2960306	minor	-1.226768	0.0202187	0.5416681	-5.064398	2.765993	0.450023	0.799368
ACE	Model 5	G	rs4277404	major	-0.0230756	0.0099856	0.981566	-1.960746	1.952891	0.5395734	0.799368
ACE	Model 5	A	rs4277404	minor	5.088464	0.0796978	0.5335866	-10.109	22.8553	0.5395734	0.799368
ACE	Model 5	A	rs4351	major	-0.6579888	0.0151942	0.6640317	-3.572789	2.34492	0.502662	0.799368
ACE	Model 5	G	rs4351	minor	1.085661	0.0173091	0.5328764	-2.286179	4.573854	0.502662	0.799368
ACE	Model 5	G	rs4353	major	-0.6723348	0.0157524	0.6685578	-3.692136	2.442154	0.5311769	0.799368
ACE	Model 5	A	rs4353	minor	0.9182478	0.0162519	0.5739486	-2.245656	4.184554	0.5311769	0.799368
ACE	Model 5	G	rs4359	major	-0.6935335	0.0149931	0.6426207	-3.569291	2.267985	0.490333	0.799368
ACE	Model 5	A	rs4359	minor	1.070166	0.0171661	0.5353303	-2.273766	4.528517	0.490333	0.799368
ACE	Model 5	G	rs4362	major	-0.7898002	0.0148557	0.5936282	-3.636824	2.141338	0.4292724	0.799368
ACE	Model 5	A	rs4362	minor	1.228121	0.0172716	0.4798965	-2.141265	4.713519	0.4292724	0.799368
EDN1	Model 5	C	rs5370	major	-0.4055494	0.0120355	0.7357002	-2.727399	1.971721	0.4531874	0.799368
EDN1	Model 5	A	rs5370	minor	1.910488	0.0255096	0.4583444	-3.059547	7.135331	0.4531874	0.799368
PTGS1	Model 5	C	rs5788	major	0.5696046	0.0116971	0.6273721	-1.70982	2.901891	0.4840758	0.799368
PTGS1	Model 5	A	rs5788	minor	-1.313144	0.0227351	0.5610955	-5.614095	3.183791	0.4840758	0.799368
VEGFA	Model 5	C	rs833060	major	0.6926584	0.0128099	0.5901071	-1.803963	3.252756	0.5102429	0.799368
VEGFA	Model 5	A	rs833060	minor	-1.156393	0.0221152	0.5990452	-5.349242	3.22219	0.5102429	0.799368
PTGS1	Model 5	G	rs876567	major	0.214843	0.009924	0.8288326	-1.715572	2.183173	0.5120612	0.799368
PTGS1	Model 5	A	rs876567	minor	-4.749403	0.0761117	0.5227689	-17.94949	10.57429	0.5120612	0.799368
ALOX15	Model 5	G	rs9894225	major	0.6124342	0.0117594	0.6037264	-1.679968	2.958285	0.4409381	0.799368
ALOX15	Model 5	A	rs9894225	minor	-1.520094	0.0233553	0.5120695	-5.926446	3.092649	0.4409381	0.799368
AGTR1	Model 5	A	rs422858	major	-0.2189972	0.0114574	0.8482909	-2.434725	2.04705	0.5509667	0.8045863
AGTR1	Model 5	C	rs422858	minor	1.823728	0.0296084	0.5417359	-3.917064	7.907524	0.5509667	0.8045863
VEGFA	Model 5	A	rs3025010	major	0.673382	0.0136296	0.6225443	-1.980364	3.398975	0.5695559	0.8086287
VEGFA	Model 5	G	rs3025010	minor	-0.8953571	0.0205327	0.6614603	-4.804468	3.174277	0.5695559	0.8086287
EDN1	Model 5	A	rs3087459	major	-0.2319729	0.0116801	0.842431	-2.489967	2.078309	0.5663716	0.8086287
EDN1	Model 5	C	rs3087459	minor	1.574732	0.0266948	0.5584745	-3.603105	7.03069	0.5663716	0.8086287
PTGS1	Model 5	G	rs1213266	major	-0.1901257	0.0112784	0.8660386	-2.372237	2.040759	0.6057241	0.8128685
PTGS1	Model 5	A	rs1213266	minor	1.359349	0.0260515	0.6043789	-3.686152	6.669165	0.6057241	0.8128685
PTGS1	Model 5	A	rs1330344	major	0.5620795	0.0132372	0.6720722	-2.013402	3.205255	0.5905326	0.8128685
PTGS1	Model 5	G	rs1330344	minor	-0.8385309	0.0196683	0.6686465	-4.588385	3.0587	0.5905326	0.8128685
EDN1	Model 5	G	rs1476046	major	-0.2749798	0.0122051	0.8215519	-2.632256	2.139366	0.5826911	0.8128685
EDN1	Model 5	A	rs1476046	minor	1.383668	0.0246724	0.5776717	-3.402293	6.406751	0.5826911	0.8128685
PTGS1	Model 5	G	rs2282169	major	0.5180092	0.0120645	0.6685556	-1.83096	2.923184	0.620254	0.8128685
PTGS1	Model 5	C	rs2282169	minor	-0.8336241	0.0224303	0.7090731	-5.098802	3.623245	0.620254	0.8128685
ACE	Model 5	G	rs4309	major	-0.4709684	0.0152912	0.7575932	-3.409612	2.55708	0.6173385	0.8128685
ACE	Model 5	A	rs4309	minor	0.7982302	0.0167312	0.6347505	-2.453589	4.158453	0.6173385	0.8128685
VEGFA	Model 5	C	rs699947	major	0.6121567	0.0134107	0.6491529	-1.997932	3.29176	0.6168361	0.8128685
VEGFA	Model 5	A	rs699947	minor	-0.7388114	0.0202911	0.7148472	-4.608945	3.288338	0.6168361	0.8128685
PTGS1	Model 5	G	rs10306202	major	0.2998166	0.0111123	0.7876759	-1.861068	2.508281	0.7081842	0.8255944
PTGS1	Model 5	A	rs10306202	minor	-0.9202966	0.0290445	0.7503054	-6.40299	4.88356	0.7081842	0.8255944
TLR4	Model 5	A	rs1927914	major	-0.2764286	0.0148355	0.8520223	-3.134346	2.665808	0.7272563	0.8255944
TLR4	Model 5	G	rs1927914	minor	0.5752676	0.0164078	0.7267118	-2.60765	3.862207	0.7272563	0.8255944

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 5	G	rs2131127	major	-0.3445359	0.0146999	0.8144247	-3.174776	2.568434	0.6594533	0.8255944
AGTR1	Model 5	A	rs2131127	minor	0.7774552	0.0174053	0.6564525	-2.602464	4.274666	0.6594533	0.8255944
TLR4	Model 5	C	rs2149356	major	-0.2924482	0.0146603	0.8416974	-3.116649	2.614079	0.7175735	0.8255944
TLR4	Model 5	A	rs2149356	minor	0.594413	0.0166744	0.7223454	-2.64	3.936277	0.7175735	0.8255944
GRK4	Model 5	A	rs2471347	major	0.479797	0.0137245	0.7273458	-2.187026	3.219329	0.6938192	0.8255944
GRK4	Model 5	G	rs2471347	minor	-0.5666282	0.0195399	0.7712571	-4.30268	3.31528	0.6938192	0.8255944
ACE	Model 5	C	rs4303	major	0.0287165	0.0099107	0.9768935	-1.895557	1.990733	0.7384247	0.8255944
ACE	Model 5	A	rs4303	minor	3.031438	0.0873343	0.7324615	-13.17782	22.26688	0.7384247	0.8255944
ACE	Model 5	A	rs4316	major	-0.3588544	0.0157771	0.8198007	-3.392866	2.770443	0.6931562	0.8255944
ACE	Model 5	G	rs4316	minor	0.6668542	0.0167026	0.6907699	-2.575271	4.016872	0.6931562	0.8255944
ACE	Model 5	A	rs4363	major	-0.4143195	0.0149155	0.7807975	-3.283448	2.539923	0.6474727	0.8255944
ACE	Model 5	G	rs4363	minor	0.7526641	0.0172149	0.6632364	-2.590083	4.210122	0.6474727	0.8255944
PTGS1	Model 5	A	rs4836885	major	0.3473887	0.011613	0.7652928	-1.910829	2.657595	0.743035	0.8255944
PTGS1	Model 5	G	rs4836885	minor	-0.5584784	0.0234598	0.8113681	-5.027312	4.120631	0.743035	0.8255944
TLR4	Model 5	G	rs4986791	major	0.0118634	0.009982	0.9905205	-1.925786	1.987795	0.6917387	0.8255944
TLR4	Model 5	A	rs4986791	minor	3.003692	0.0728548	0.6846725	-10.70263	18.81381	0.6917387	0.8255944
VEGFB	Model 5	G	rs594942	major	-0.2109413	0.013384	0.8746676	-2.794593	2.441382	0.6946835	0.8255944
VEGFB	Model 5	A	rs594942	minor	0.8528606	0.0203296	0.6762285	-3.086635	4.952495	0.6946835	0.8255944
AGT	Model 5	A	rs7536290	major	0.354068	0.012259	0.773167	-2.02842	2.794493	0.7325659	0.8255944
AGT	Model 5	G	rs7536290	minor	-0.6430405	0.0238597	0.7869247	-5.182424	4.113665	0.7325659	0.8255944
ACE	Model 5	A	rs8066276	major	0.497762	0.014639	0.7345458	-2.344744	3.423006	0.7230473	0.8255944
ACE	Model 5	G	rs8066276	minor	-0.423134	0.0179351	0.8131519	-3.862671	3.13946	0.7230473	0.8255944
VEGFA	Model 5	A	rs833069	major	0.4153758	0.0148088	0.7796038	-2.457268	3.372619	0.7428496	0.8255944
VEGFA	Model 5	G	rs833069	minor	-0.4239626	0.0174577	0.8077704	-3.773466	3.042132	0.7428496	0.8255944
ALOX15	Model 5	A	rs2255888	major	0.2917881	0.0120392	0.8088204	-2.047031	2.686451	0.7866375	0.8530318
ALOX15	Model 5	G	rs2255888	minor	-0.427531	0.0218398	0.8445113	-4.599813	3.927224	0.7866375	0.8530318
AGTR1	Model 5	A	rs2320019	major	0.0708435	0.0106699	0.9470949	-2.000172	2.185625	0.8011081	0.8530318
AGTR1	Model 5	G	rs2320019	minor	0.9895259	0.0333798	0.7680647	-5.406037	7.817497	0.8011081	0.8530318
AGTR1	Model 5	A	rs409742	major	-0.0216921	0.0115107	0.9849668	-2.252009	2.259514	0.7976223	0.8530318
AGTR1	Model 5	G	rs409742	minor	0.8350595	0.0288484	0.7732055	-4.708151	6.700724	0.7976223	0.8530318
AGTR1	Model 5	G	rs4681443	major	-0.0945348	0.0117972	0.9361175	-2.378064	2.24241	0.798116	0.8530318
AGTR1	Model 5	A	rs4681443	minor	0.5706987	0.0216674	0.7928813	-3.610858	4.93366	0.798116	0.8530318
ADRB2	Model 5	G	rs1042713	major	0.3961927	0.0151706	0.7944219	-2.545022	3.426174	0.8111016	0.8547692
ADRB2	Model 5	A	rs1042713	minor	-0.2077345	0.0167457	0.9011964	-3.429839	3.121877	0.8111016	0.8547692
GRK4	Model 5	C	rs1008210	major	0.2501478	0.0139674	0.8580757	-2.457035	3.032465	0.8902149	0.8578721
GRK4	Model 5	A	rs1008210	minor	-0.1163759	0.0191964	0.9516428	-3.804597	3.713255	0.8902149	0.8578721
TLR4	Model 5	A	rs1927906	major	0.1716347	0.0110004	0.8761497	-1.964989	2.354825	0.8532163	0.8578721
TLR4	Model 5	G	rs1927906	minor	-0.417021	0.0284885	0.8834078	-5.824997	5.301507	0.8532163	0.8578721
TLR4	Model 5	G	rs1927911	major	-0.0672262	0.0138167	0.9611903	-2.73711	2.675946	0.860879	0.8578721
TLR4	Model 5	A	rs1927911	minor	0.3827547	0.018603	0.8373356	-3.211396	4.11037	0.860879	0.8578721
GRK4	Model 5	A	rs2798298	major	0.2215179	0.0140843	0.8751931	-2.507234	3.026646	0.9079852	0.8578721
GRK4	Model 5	G	rs2798298	minor	-0.083013	0.0188796	0.9649227	-3.712699	3.683499	0.9079852	0.8578721
GRK4	Model 5	A	rs2857844	major	-0.0472396	0.0152695	0.97532	-2.994283	2.989335	0.8764591	0.8578721
GRK4	Model 5	G	rs2857844	minor	0.3306064	0.0158757	0.8353473	-2.743199	3.501559	0.8764591	0.8578721
ACE	Model 5	G	rs4295	major	0.2581109	0.0135662	0.8493361	-2.372554	2.959662	0.8783579	0.8578721
ACE	Model 5	C	rs4295	minor	-0.1551479	0.0200797	0.9383797	-4.008273	3.852643	0.8783579	0.8578721

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ACE	Model 5	G	rs4311	major	-0.0350971	0.0137667	0.9796624	-2.696316	2.698905	0.8865809	0.8578721
ACE	Model 5	A	rs4311	minor	0.3515079	0.0198947	0.8600354	-3.486176	4.341789	0.8865809	0.8578721
ACE	Model 5	A	rs4459610	major	0.3411871	0.0150277	0.8207403	-2.571134	3.340563	0.8511019	0.8578721
ACE	Model 5	T	rs4459610	minor	-0.137096	0.0170753	0.9359797	-3.423901	3.26157	0.8511019	0.8578721
ACE	Model 5	A	rs4968591	major	0.1866309	0.0123302	0.8798326	-2.205526	2.637303	0.9147528	0.8578721
ACE	Model 5	G	rs4968591	minor	-0.1202062	0.0232504	0.9587528	-4.569572	4.536608	0.9147528	0.8578721
AGTR1	Model 5	G	rs718858	major	0.0484775	0.0110007	0.9648679	-2.085584	2.229051	0.8335151	0.8578721
AGTR1	Model 5	A	rs718858	minor	0.8079448	0.0324	0.8039039	-5.394615	7.417159	0.8335151	0.8578721
VEGFA	Model 5	G	rs735286	major	0.1957335	0.0128157	0.8787606	-2.28966	2.744346	0.9075825	0.8578721
VEGFA	Model 5	A	rs735286	minor	-0.1306679	0.0220826	0.9527962	-4.360924	4.286699	0.9075825	0.8578721
PTGS1	Model 5	G	rs883484	major	0.2478	0.0123621	0.8413621	-2.151939	2.706393	0.8258549	0.8578721
PTGS1	Model 5	A	rs883484	minor	-0.3722759	0.0227921	0.8700473	-4.724867	4.179161	0.8258549	0.8578721
GRK4	Model 5	G	rs1801058	major	0.0596224	0.0138498	0.965681	-2.619967	2.812946	0.9613174	0.8696283
GRK4	Model 5	A	rs1801058	minor	0.1881914	0.019287	0.9223626	-3.528408	4.047973	0.9613174	0.8696283
TLR4	Model 5	A	rs2737191	major	0.1481666	0.0109887	0.8928483	-1.985712	2.328501	0.9608834	0.8696283
TLR4	Model 5	G	rs2737191	minor	-0.0174003	0.0302743	0.9954149	-5.777433	6.094756	0.9608834	0.8696283
ACE	Model 5	T	rs4291	major	0.0556994	0.0133478	0.966732	-2.527929	2.70781	0.9586192	0.8696283
ACE	Model 5	A	rs4291	minor	0.1959334	0.0203612	0.9234329	-3.723871	4.27533	0.9586192	0.8696283
ACE	Model 5	G	rs4461142	major	0.0416127	0.0135904	0.9755844	-2.58798	2.74219	0.9514219	0.8696283
ACE	Model 5	A	rs4461142	minor	0.202353	0.019494	0.91743	-3.553917	4.104918	0.9514219	0.8696283
ADRB2	Model 1	C	rs1042719	major	1.093816	0.0147595	0.4612604	-1.788748	4.060985	0.2812939	0.880418
ADRB2	Model 1	G	rs1042719	minor	-1.908841	0.0202247	0.3408644	-5.721095	2.057565	0.2812939	0.880418
VEGFA	Model 1	C	rs1109324	major	-0.8456929	0.0115039	0.4605303	-3.056339	1.415364	0.1012522	0.880418
VEGFA	Model 1	A	rs1109324	minor	5.978737	0.0369236	0.1161146	-1.419892	13.93265	0.1012522	0.880418
TLR4	Model 1	G	rs11536889	major	0.8014863	0.0116214	0.4922941	-1.468562	3.123833	0.1165396	0.880418
TLR4	Model 1	C	rs11536889	minor	-5.32981	0.0360914	0.1294408	-11.7952	1.60949	0.1165396	0.880418
PTGS1	Model 1	G	rs1213266	major	-0.7861553	0.0119506	0.5091242	-3.083003	1.565125	0.2179854	0.880418
PTGS1	Model 1	A	rs1213266	minor	3.152153	0.0275402	0.2600575	-2.268168	8.873092	0.2179854	0.880418
ADRB2	Model 1	G	rs12654778	major	-1.052947	0.013843	0.4446487	-3.701457	1.668405	0.276935	0.880418
ADRB2	Model 1	A	rs12654778	minor	2.129539	0.0223901	0.3468697	-2.255371	6.711159	0.276935	0.880418
VEGFA	Model 1	G	rs1413711	major	1.41605	0.0143787	0.3283525	-1.402128	4.314779	0.146373	0.880418
VEGFA	Model 1	A	rs1413711	minor	-2.738066	0.0213909	0.194636	-6.731512	1.426366	0.146373	0.880418
EDN1	Model 1	G	rs1476046	major	-0.8526216	0.0129556	0.5088069	-3.338518	1.697206	0.2969177	0.880418
EDN1	Model 1	A	rs1476046	minor	2.503964	0.0261778	0.3450198	-2.622631	7.900456	0.2969177	0.880418
VEGFA	Model 1	T	rs1547651	major	-0.9244956	0.0115444	0.4212739	-3.141059	1.342793	0.0866376	0.880418
VEGFA	Model 1	A	rs1547651	minor	6.115731	0.0363029	0.1023362	-1.172299	13.94122	0.0866376	0.880418
EDN1	Model 1	G	rs1630736	major	1.9049	0.0145036	0.1935423	-0.9511108	4.843261	0.0583595	0.880418
EDN1	Model 1	A	rs1630736	minor	-3.007957	0.0189346	0.1070639	-6.541471	0.6591541	0.0583595	0.880418
PTGS1	Model 1	G	rs1888943	major	-0.6521375	0.0108481	0.5465642	-2.742162	1.482801	0.0616714	0.880418
PTGS1	Model 1	A	rs1888943	minor	9.05619	0.0476205	0.0689837	-0.6619335	19.72503	0.0616714	0.880418
GRK4	Model 1	G	rs2105380	major	-0.3258183	0.010542	0.7569525	-2.364159	1.755077	0.2029307	0.880418
GRK4	Model 1	A	rs2105380	minor	10.57003	0.0799291	0.2090116	-5.46304	29.32225	0.2029307	0.880418
AGTR1	Model 1	G	rs2131127	major	-1.217866	0.0156001	0.4323631	-4.19248	1.849104	0.2944694	0.880418
AGTR1	Model 1	A	rs2131127	minor	1.608646	0.0183727	0.3852763	-1.985163	5.334226	0.2944694	0.880418
AGTR1	Model 1	A	rs2320019	major	-0.4764956	0.011317	0.6730795	-2.659718	1.755694	0.2657686	0.880418
AGTR1	Model 1	G	rs2320019	minor	3.835909	0.0349747	0.282074	-3.043477	11.20341	0.2657686	0.880418

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 1	A	rs2638360	major	-0.6946955	0.0113021	0.5375053	-2.870301	1.529641	0.157584	0.880418
AGTR1	Model 1	G	rs2638360	minor	5.575713	0.0400135	0.1754073	-2.387723	14.18883	0.157584	0.880418
AGTR1	Model 1	A	rs275645	major	-1.745617	0.0164069	0.2833738	-4.854913	1.46529	0.1693914	0.880418
AGTR1	Model 1	G	rs275645	minor	1.884537	0.0170809	0.274644	-1.469893	5.353167	0.1693914	0.880418
AGTR1	Model 1	G	rs275646	major	0.5090869	0.0110118	0.6447991	-1.636923	2.701917	0.2006524	0.880418
AGTR1	Model 1	A	rs275646	minor	-5.915189	0.0487956	0.2117492	-14.49635	3.527183	0.2006524	0.880418
VEGFA	Model 1	A	rs3025033	major	0.6274303	0.012104	0.6054479	-1.731703	3.0432	0.2954722	0.880418
VEGFA	Model 1	G	rs3025033	minor	-2.907765	0.0296747	0.3202644	-8.393694	2.906693	0.2954722	0.880418
VEGFA	Model 1	G	rs3025035	major	0.5646366	0.0116788	0.629833	-1.711149	2.893116	0.2310377	0.880418
VEGFA	Model 1	A	rs3025035	minor	-3.701112	0.0323818	0.244439	-9.62301	2.608815	0.2310377	0.880418
AGT	Model 1	G	rs3789670	major	-0.8446833	0.0119201	0.476858	-3.134385	1.499142	0.1797031	0.880418
AGT	Model 1	A	rs3789670	minor	4.095957	0.0319687	0.2095207	-2.226304	10.82703	0.1797031	0.880418
AGT	Model 1	C	rs3789671	major	-1.111128	0.014083	0.4277327	-3.803349	1.65644	0.2684872	0.880418
AGT	Model 1	A	rs3789671	minor	1.955787	0.020757	0.3509763	-2.108837	6.189182	0.2684872	0.880418
PTGS1	Model 1	G	rs3842787	major	0.2973793	0.0108161	0.7837306	-1.806453	2.446287	0.2556002	0.880418
PTGS1	Model 1	A	rs3842787	minor	-6.244675	0.0569879	0.2581168	-16.15295	4.83447	0.2556002	0.880418
ACE	Model 1	C	rs4303	major	-0.2667949	0.0104877	0.7989846	-2.295928	1.80448	0.3012766	0.880418
ACE	Model 1	A	rs4303	minor	9.85067	0.0920938	0.3078956	-8.290915	31.58096	0.3012766	0.880418
PTGS2	Model 1	C	rs4648307	major	-0.6318246	0.0113738	0.5774686	-2.822464	1.608198	0.2213587	0.880418
PTGS2	Model 1	A	rs4648307	minor	4.742179	0.0396	0.2422837	-3.079868	13.19551	0.2213587	0.880418
EDN1	Model 1	C	rs5370	major	-0.8962415	0.0127835	0.4814402	-3.348461	1.618195	0.2545594	0.880418
EDN1	Model 1	A	rs5370	minor	2.85257	0.0270573	0.2988183	-2.459739	8.454202	0.2545594	0.880418
ALOX15	Model 1	G	rs6502804	major	1.41014	0.0168109	0.4050637	-1.876753	4.807136	0.281541	0.880418
ALOX15	Model 1	A	rs6502804	minor	-1.52995	0.0174073	0.3759893	-4.832856	1.887586	0.281541	0.880418
GRK4	Model 1	A	rs6846128	major	-0.5186883	0.0107053	0.6272312	-2.584253	1.590674	0.0887337	0.880418
GRK4	Model 1	G	rs6846128	minor	11.07477	0.0626966	0.0941958	-1.769139	25.59805	0.0887337	0.880418
AGT	Model 1	G	rs699	major	0.8552209	0.0136214	0.5319935	-1.801723	3.584053	0.3020323	0.880418
AGT	Model 1	A	rs699	minor	-1.93094	0.020927	0.3517019	-5.871975	2.175102	0.3020323	0.880418
VEGFA	Model 1	A	rs699946	major	0.9592662	0.0131213	0.467034	-1.604027	3.589335	0.2352975	0.880418
VEGFA	Model 1	G	rs699946	minor	-2.674984	0.0249889	0.2781633	-7.32686	2.210401	0.2352975	0.880418
ALOX15	Model 1	G	rs7217186	major	-1.761219	0.0161046	0.2701392	-4.813652	1.389099	0.149652	0.880418
ALOX15	Model 1	A	rs7217186	minor	2.097384	0.0176722	0.2404548	-1.378412	5.695681	0.149652	0.880418
ALOX15	Model 1	C	rs7220870	major	-1.3225	0.0122765	0.2784276	-3.668489	1.080622	0.0474552	0.880418
ALOX15	Model 1	A	rs7220870	minor	5.819551	0.0303469	0.0626221	-0.2909475	12.30452	0.0474552	0.880418
ACE	Model 1	A	rs8066276	major	1.388128	0.0155406	0.3752504	-1.653506	4.523833	0.2240606	0.880418
ACE	Model 1	G	rs8066276	minor	-1.953441	0.0189658	0.2985138	-5.531145	1.759757	0.2240606	0.880418
PTGS1	Model 1	G	rs876567	major	0.2219277	0.0105023	0.8328683	-1.819963	2.306285	0.1926259	0.880418
PTGS1	Model 1	A	rs876567	minor	-9.934084	0.0805315	0.1941676	-23.08484	5.465162	0.1926259	0.880418
ALOX15	Model 1	A	rs916055	major	1.256105	0.0139145	0.3698787	-1.468035	4.055561	0.1661769	0.880418
ALOX15	Model 1	G	rs916055	minor	-2.755135	0.0223443	0.2114687	-6.921979	1.598247	0.1661769	0.880418
AGT	Model 1	G	rs943580	major	0.9357049	0.0135561	0.4922205	-1.710798	3.653467	0.2625541	0.880418
AGT	Model 1	A	rs943580	minor	-2.122723	0.0213007	0.3140435	-6.124832	2.050005	0.2625541	0.880418
ACE	Model 5	G	rs4305	major	0.114298	0.0155873	0.9415934	-2.898001	3.220044	0.9843427	0.8826465
ACE	Model 5	A	rs4305	minor	0.065318	0.0160847	0.9676266	-3.040085	3.27018	0.9843427	0.8826465
AGT	Model 5	G	rs2478545	major	0.1213995	0.0128814	0.9249794	-2.374723	2.681344	0.9989696	0.887973
AGT	Model 5	A	rs2478545	minor	0.117997	0.0203594	0.9538217	-3.798423	4.193856	0.9989696	0.887973

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
GRK4	Model 1	G	rs1024323	major	0.9162382	0.0148158	0.538296	-1.972069	3.889647	0.3481914	0.896951
GRK4	Model 1	A	rs1024323	minor	-1.60747	0.0193282	0.4019918	-5.26512	2.191398	0.3481914	0.896951
ADRB2	Model 1	G	rs11168070	major	-0.696222	0.0124303	0.574203	-3.086329	1.752831	0.3346515	0.896951
ADRB2	Model 1	C	rs11168070	minor	2.292503	0.0259212	0.3820959	-2.77462	7.623711	0.3346515	0.896951
GRK4	Model 1	A	rs2488813	major	0.6502732	0.0128568	0.6142721	-1.854316	3.218777	0.3426732	0.896951
GRK4	Model 1	T	rs2488813	minor	-2.259072	0.0254231	0.3689872	-7.010002	2.734587	0.3426732	0.896951
VEGFA	Model 1	C	rs699947	major	0.8969373	0.0141945	0.5294461	-1.871409	3.743382	0.3434263	0.896951
VEGFA	Model 1	A	rs699947	minor	-1.808316	0.0215342	0.39696	-5.866376	2.424685	0.3434263	0.896951
ALOX15	Model 1	A	rs743646	major	-0.3693528	0.0107983	0.7319107	-2.455804	1.761727	0.3207956	0.896951
ALOX15	Model 1	G	rs743646	minor	5.795074	0.0581522	0.3329148	-5.60126	18.56724	0.3207956	0.896951
GRK4	Model 1	C	rs1008210	major	0.3931296	0.0147592	0.7904167	-2.469383	3.339657	0.6511989	0.9150152
GRK4	Model 1	A	rs1008210	minor	-0.8747251	0.0203552	0.6661108	-4.751535	3.159879	0.6511989	0.9150152
GRK4	Model 1	C	rs1056094	major	0.3035012	0.0137312	0.8253749	-2.359936	3.039593	0.6833335	0.9150152
GRK4	Model 1	G	rs1056094	minor	-0.8271549	0.0213688	0.6975845	-4.89494	3.414615	0.6833335	0.9150152
PTGS2	Model 1	A	rs10911905	major	-0.3257222	0.0114457	0.7756691	-2.536839	1.935558	0.5557395	0.9150152
PTGS2	Model 1	C	rs10911905	minor	2.12079	0.0375761	0.5766304	-5.129909	9.925644	0.5557395	0.9150152
PTGS1	Model 1	G	rs10985620	major	0.1105026	0.0105954	0.9170036	-1.947017	2.211197	0.4991248	0.9150152
PTGS1	Model 1	C	rs10985620	minor	-4.51316	0.068228	0.4986427	-16.46514	9.148879	0.4991248	0.9150152
PTGS1	Model 1	A	rs1330344	major	0.5403329	0.0140312	0.7010184	-2.186924	3.343632	0.5253409	0.9150152
PTGS1	Model 1	G	rs1330344	minor	-1.215085	0.0209104	0.5589148	-5.181808	2.917586	0.5253409	0.9150152
GRK4	Model 1	A	rs1419046	major	0.3182379	0.0137533	0.8173447	-2.349819	3.059194	0.6734487	0.9150152
GRK4	Model 1	T	rs1419046	minor	-0.8481327	0.0213028	0.6893669	-4.902752	3.379362	0.6734487	0.9150152
ALOX15	Model 1	A	rs1871346	major	0.0813603	0.0106821	0.939328	-1.992223	2.198815	0.6460668	0.9150152
ALOX15	Model 1	G	rs1871346	minor	-2.633954	0.0579858	0.6453791	-13.09396	9.08502	0.6460668	0.9150152
TLR4	Model 1	G	rs1927907	major	0.4483133	0.0121689	0.7132605	-1.919098	2.872868	0.4051628	0.9150152
TLR4	Model 1	A	rs1927907	minor	-2.381239	0.0296783	0.4169527	-7.897578	3.465492	0.4051628	0.9150152
TLR4	Model 1	G	rs1927911	major	-0.620349	0.0146443	0.6709785	-3.432224	2.273403	0.5964631	0.9150152
TLR4	Model 1	A	rs1927911	minor	0.8211605	0.0197047	0.6782087	-2.998382	4.791101	0.5964631	0.9150152
TLR4	Model 1	A	rs1927914	major	-1.004235	0.0157586	0.5220066	-4.015117	2.101093	0.4171283	0.9150152
TLR4	Model 1	G	rs1927914	minor	1.091273	0.0172985	0.5305203	-2.278717	4.577479	0.4171283	0.9150152
AGT	Model 1	G	rs2148582	major	0.6038424	0.0135538	0.6570116	-2.033506	3.312191	0.4358065	0.9150152
AGT	Model 1	A	rs2148582	minor	-1.510792	0.0211239	0.4712852	-5.505185	2.652448	0.4358065	0.9150152
TLR4	Model 1	C	rs2149356	major	-0.9549392	0.0155709	0.5378811	-3.93197	2.114346	0.4381259	0.9150152
TLR4	Model 1	A	rs2149356	minor	1.056196	0.0175895	0.5504297	-2.368333	4.600843	0.4381259	0.9150152
ALOX15	Model 1	A	rs2255888	major	-0.3466938	0.012768	0.7856745	-2.809557	2.178579	0.6435071	0.9150152
ALOX15	Model 1	G	rs2255888	minor	0.9546725	0.0229794	0.6793467	-3.491335	5.605501	0.6435071	0.9150152
PTGS1	Model 1	G	rs2282169	major	0.5076122	0.0128151	0.6928522	-1.985417	3.064052	0.5461712	0.9150152
PTGS1	Model 1	C	rs2282169	minor	-1.236137	0.0237325	0.6003186	-5.724908	3.466359	0.5461712	0.9150152
GRK4	Model 1	G	rs2471327	major	0.5522859	0.0149854	0.7132984	-2.358078	3.549398	0.5497257	0.9150152
GRK4	Model 1	A	rs2471327	minor	-1.052055	0.019034	0.5785736	-4.6754	2.709015	0.5497257	0.9150152
GRK4	Model 1	A	rs2471337	major	0.3262634	0.0136075	0.8108625	-2.314096	3.037989	0.6342116	0.9150152
GRK4	Model 1	G	rs2471337	minor	-1.016354	0.0219966	0.6424523	-5.193112	3.344413	0.6342116	0.9150152
GRK4	Model 1	A	rs2471347	major	0.5558668	0.0145037	0.7023972	-2.26237	3.455366	0.5261803	0.9150152
GRK4	Model 1	G	rs2471347	minor	-1.224936	0.0207356	0.5523864	-5.158772	2.872067	0.5261803	0.9150152
GRK4	Model 1	A	rs2488806	major	0.3277282	0.015049	0.8279267	-2.588266	3.331012	0.6833609	0.9150152
GRK4	Model 1	C	rs2488806	minor	-0.7682831	0.0189959	0.6848237	-4.39488	2.995882	0.6833609	0.9150152

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
GRK4	Model 1	G	rs2488815	major	0.6619532	0.0149203	0.6584418	-2.239101	3.649096	0.4627469	0.9150152
GRK4	Model 1	A	rs2488815	minor	-1.306136	0.0191071	0.4915566	-4.9338	2.459958	0.4627469	0.9150152
AGTR1	Model 1	G	rs2638363	major	-0.4503269	0.0124391	0.7167993	-2.848022	2.006542	0.5036311	0.9150152
AGTR1	Model 1	A	rs2638363	minor	1.716053	0.0272574	0.5326169	-3.575366	7.297845	0.5036311	0.9150152
GRK4	Model 1	A	rs2798298	major	0.4775053	0.0148771	0.7488815	-2.409972	3.450417	0.59624	0.9150152
GRK4	Model 1	G	rs2798298	minor	-0.9951276	0.0200004	0.6171522	-4.801034	2.962934	0.59624	0.9150152
GRK4	Model 1	A	rs2857844	major	-1.01596	0.0162117	0.5289108	-4.111664	2.179687	0.4285732	0.9150152
GRK4	Model 1	G	rs2857844	minor	1.020937	0.0167689	0.5448241	-2.245289	4.396296	0.4285732	0.9150152
GRK4	Model 1	A	rs2960298	major	0.318763	0.013576	0.8147029	-2.315367	3.023925	0.6436667	0.9150152
GRK4	Model 1	G	rs2960298	minor	-0.985621	0.0220196	0.6529298	-5.167947	3.381156	0.6436667	0.9150152
GRK4	Model 1	G	rs3021140	major	0.3932176	0.0135621	0.7723578	-2.240196	3.097569	0.5795068	0.9150152
GRK4	Model 1	A	rs3021140	minor	-1.161142	0.0219191	0.5942639	-5.317412	3.177575	0.5795068	0.9150152
EDN1	Model 1	A	rs3087459	major	-0.5293715	0.0123982	0.6686642	-2.917377	1.917374	0.4610896	0.9150152
EDN1	Model 1	C	rs3087459	minor	1.943306	0.0283629	0.4975579	-3.569109	7.770835	0.4610896	0.9150152
AGTR1	Model 1	G	rs3772616	major	0.7768417	0.0136104	0.569779	-1.875929	3.50133	0.3690514	0.9150152
AGTR1	Model 1	A	rs3772616	minor	-1.497833	0.0195013	0.4391851	-5.191718	2.339971	0.3690514	0.9150152
AGTR1	Model 1	A	rs422858	major	-0.2589463	0.012109	0.8304944	-2.598251	2.136541	0.6809624	0.9150152
AGTR1	Model 1	C	rs422858	minor	1.224899	0.0312949	0.6973392	-4.797348	7.628097	0.6809624	0.9150152
ACE	Model 1	A	rs4351	major	-0.8407949	0.0161447	0.6010982	-3.929369	2.347074	0.5113519	0.9150152
ACE	Model 1	G	rs4351	minor	0.97366	0.0183543	0.5976761	-2.594186	4.672191	0.5113519	0.9150152
ACE	Model 1	G	rs4353	major	-0.9357748	0.0167166	0.573954	-4.128914	2.363718	0.4996551	0.9150152
ACE	Model 1	A	rs4353	minor	0.8804255	0.0171964	0.6103446	-2.463016	4.338476	0.4996551	0.9150152
ACE	Model 1	G	rs4359	major	-0.6830452	0.0158808	0.6661376	-3.72675	2.456887	0.6035212	0.9150152
ACE	Model 1	A	rs4359	minor	0.7214668	0.0181702	0.6924593	-2.802406	4.373096	0.6035212	0.9150152
ACE	Model 1	G	rs4362	major	-0.829006	0.015739	0.5969815	-3.84152	2.277886	0.5147541	0.9150152
ACE	Model 1	A	rs4362	minor	0.9318917	0.0183017	0.6123894	-2.624439	4.618105	0.5147541	0.9150152
ACE	Model 1	A	rs4363	major	-0.6087456	0.0157915	0.6990849	-3.637865	2.515593	0.640908	0.9150152
ACE	Model 1	G	rs4363	minor	0.6509346	0.0182347	0.7220517	-2.882749	4.313194	0.640908	0.9150152
ACE	Model 1	A	rs4459610	major	0.7175034	0.0159567	0.6542146	-2.383655	3.917182	0.5501328	0.9150152
ACE	Model 1	T	rs4459610	minor	-0.8927179	0.018027	0.6189922	-4.333269	2.671569	0.5501328	0.9150152
AGTR1	Model 1	G	rs4488792	major	0.5036302	0.0131846	0.7032653	-2.060244	3.134622	0.5158653	0.9150152
AGTR1	Model 1	A	rs4488792	minor	-1.243864	0.0214395	0.5594778	-5.307676	2.994349	0.5158653	0.9150152
AGTR1	Model 1	G	rs4681443	major	-0.5178096	0.0125409	0.6789852	-2.933244	1.957731	0.4643412	0.9150152
AGTR1	Model 1	A	rs4681443	minor	1.500928	0.0228278	0.5141555	-2.940303	6.145379	0.4643412	0.9150152
TLR4	Model 1	G	rs4986791	major	-0.1758853	0.0105691	0.8677488	-2.222472	1.913539	0.5758879	0.9150152
TLR4	Model 1	A	rs4986791	minor	4.32942	0.0772604	0.5834189	-10.33093	21.38665	0.5758879	0.9150152
PTGS1	Model 1	C	rs5788	major	0.3338305	0.0124224	0.7885351	-2.079542	2.806684	0.6232467	0.9150152
PTGS1	Model 1	A	rs5788	minor	-1.066994	0.0240271	0.6553579	-5.617974	3.703428	0.6232467	0.9150152
ALOX15	Model 1	A	rs748694	major	0.696996	0.016463	0.673187	-2.500322	3.999164	0.5613418	0.9150152
ALOX15	Model 1	G	rs748694	minor	-0.8331107	0.0170081	0.6229103	-4.084378	2.528365	0.5613418	0.9150152
AGT	Model 1	G	rs7549009	major	-0.5422049	0.013296	0.6826974	-3.100566	2.083703	0.5460235	0.9150152
AGT	Model 1	A	rs7549009	minor	1.192996	0.0227289	0.6019434	-3.215999	5.802843	0.5460235	0.9150152
VEGFA	Model 1	A	rs833069	major	-0.6118792	0.0157087	0.6960934	-3.625267	2.495729	0.685626	0.9150152
VEGFA	Model 1	G	rs833069	minor	0.4865424	0.018492	0.793012	-3.090247	4.195345	0.685626	0.9150152
ADRB2	Model 1	G	rs1042713	major	0.4281168	0.0160566	0.790247	-2.683172	3.638876	0.7016243	0.9225873
ADRB2	Model 1	A	rs1042713	minor	-0.594117	0.0177016	0.7364662	-3.983807	2.91524	0.7016243	0.9225873

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
GRK4	Model 1	A	rs2185886	major	0.2388486	0.0152358	0.8756067	-2.710196	3.277285	0.7518037	0.9225873
GRK4	Model 1	G	rs2185886	minor	-0.5883307	0.0181914	0.745728	-4.070351	3.020079	0.7518037	0.9225873
GRK4	Model 1	C	rs2960306	major	0.242885	0.0137126	0.8596146	-2.415382	2.973565	0.7413271	0.9225873
GRK4	Model 1	A	rs2960306	minor	-0.6744782	0.0214428	0.7523625	-4.762348	3.588855	0.7413271	0.9225873
ACE	Model 1	A	rs4316	major	-0.5050467	0.0167797	0.762906	-3.723976	2.821506	0.7112472	0.9225873
ACE	Model 1	G	rs4316	minor	0.5152163	0.0176574	0.771084	-2.90389	4.054721	0.7112472	0.9225873
VEGFB	Model 1	G	rs594942	major	0.3116279	0.0142063	0.8266812	-2.442909	3.14394	0.7281208	0.9225873
VEGFB	Model 1	A	rs594942	minor	-0.6835585	0.021534	0.7501561	-4.788073	3.597898	0.7281208	0.9225873
AGTR1	Model 1	G	rs718858	major	-0.1570012	0.0116539	0.892777	-2.411693	2.149783	0.7390879	0.9225873
AGTR1	Model 1	A	rs718858	minor	1.114991	0.0341817	0.7457106	-5.437261	8.121247	0.7390879	0.9225873
AGT	Model 1	A	rs7536290	major	0.1758232	0.0129731	0.8923151	-2.33922	2.755636	0.7579311	0.9225873
AGT	Model 1	G	rs7536290	minor	-0.7785374	0.0253695	0.7580855	-5.591505	4.279796	0.7579311	0.9225873
TLR4	Model 1	C	rs7873784	major	0.1298353	0.0116831	0.9115923	-2.136938	2.449113	0.723631	0.9225873
TLR4	Model 1	G	rs7873784	minor	-1.224385	0.0345837	0.7217509	-7.697809	5.703038	0.723631	0.9225873
PTGS1	Model 1	G	rs10306202	major	-0.0868167	0.0117739	0.9412093	-2.366055	2.24563	0.9311104	0.939743
PTGS1	Model 1	A	rs10306202	minor	0.2132036	0.0307852	0.944859	-5.654646	6.446006	0.9311104	0.939743
ALOX15	Model 1	A	rs1076039	major	-0.0726699	0.0110184	0.947409	-2.207525	2.10879	0.8970972	0.939743
ALOX15	Model 1	T	rs1076039	minor	0.5858713	0.0479712	0.9031029	-8.440413	10.502	0.8970972	0.939743
AGT	Model 1	A	rs1326886	major	-0.1253296	0.0128234	0.9221136	-2.604238	2.416672	0.9085401	0.939743
AGT	Model 1	G	rs1326886	minor	0.2168655	0.0244461	0.9294052	-4.471658	5.135501	0.9085401	0.939743
TLR4	Model 1	A	rs1554973	major	0.0922499	0.0132901	0.9447005	-2.481297	2.733714	0.8261338	0.939743
TLR4	Model 1	G	rs1554973	minor	-0.4921118	0.0209901	0.8142354	-4.502794	3.687011	0.8261338	0.939743
GRK4	Model 1	G	rs1801058	major	0.141242	0.0146327	0.9231772	-2.689974	3.054832	0.8187522	0.939743
GRK4	Model 1	A	rs1801058	minor	-0.5003837	0.0204593	0.8063601	-4.411324	3.570569	0.8187522	0.939743
PTGS2	Model 1	G	rs2206593	major	0.0084647	0.0106361	0.993652	-2.054765	2.115157	0.8650428	0.939743
PTGS2	Model 1	A	rs2206593	minor	-1.273584	0.0739833	0.8624897	-14.59983	14.13216	0.8650428	0.939743
AGT	Model 1	G	rs2478545	major	-0.1829997	0.0136597	0.8933557	-2.819893	2.525443	0.8747056	0.939743
AGT	Model 1	A	rs2478545	minor	0.2586689	0.0216456	0.9050242	-3.905809	4.603625	0.8747056	0.939743
TLR4	Model 1	A	rs2737191	major	0.0337278	0.0116356	0.9768848	-2.221756	2.34124	0.9281819	0.939743
TLR4	Model 1	G	rs2737191	minor	-0.2890573	0.0321552	0.9282857	-6.379209	6.197267	0.9281819	0.939743
VEGFA	Model 1	A	rs3025010	major	0.2315803	0.014412	0.8725198	-2.560049	3.103189	0.8046155	0.939743
VEGFA	Model 1	G	rs3025010	minor	-0.4926347	0.0218077	0.8208916	-4.656191	3.852739	0.8046155	0.939743
AGTR1	Model 1	A	rs409742	major	0.0909876	0.0121673	0.9404313	-2.267686	2.506586	0.8824723	0.939743
AGTR1	Model 1	G	rs409742	minor	-0.4282745	0.0304976	0.8881113	-6.205707	5.705029	0.8824723	0.939743
ACE	Model 1	G	rs4277404	major	-0.0273525	0.0105548	0.9793276	-2.074237	2.062316	0.9437458	0.939743
ACE	Model 1	A	rs4277404	minor	-0.6355082	0.0848459	0.940118	-15.8585	17.34164	0.9437458	0.939743
ACE	Model 1	T	rs4291	major	0.0322727	0.0141641	0.9818294	-2.706551	2.848195	0.9312308	0.939743
ACE	Model 1	A	rs4291	minor	-0.2147617	0.0215615	0.9205935	-4.343801	4.092509	0.9312308	0.939743
ACE	Model 1	G	rs4305	major	-0.3325748	0.0165746	0.8407496	-3.518315	2.958356	0.8278122	0.939743
ACE	Model 1	A	rs4305	minor	0.241047	0.0169303	0.886947	-3.030647	3.623126	0.8278122	0.939743
ACE	Model 1	G	rs4309	major	-0.1327156	0.0161243	0.9343749	-3.239475	3.073794	0.9201418	0.939743
ACE	Model 1	A	rs4309	minor	0.1368878	0.0178063	0.9387794	-3.297583	3.693337	0.9201418	0.939743
ACE	Model 1	G	rs4461142	major	0.0122925	0.0143864	0.9931847	-2.768344	2.87245	0.9477934	0.939743
ACE	Model 1	A	rs4461142	minor	-0.1710236	0.0207273	0.9342006	-4.145287	3.968018	0.9477934	0.939743
PTGS1	Model 1	A	rs4836885	major	-0.0662569	0.012331	0.9571453	-2.452537	2.378398	0.9146087	0.939743
PTGS1	Model 1	G	rs4836885	minor	0.2482857	0.0247913	0.9203438	-4.506343	5.239647	0.9146087	0.939743

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ACE	Model 1	A	rs4968591	major	0.1215853	0.0130706	0.9259495	-2.410741	2.719623	0.8398439	0.939743
ACE	Model 1	G	rs4968591	minor	-0.4908808	0.0245901	0.8414302	-5.173066	4.422493	0.8398439	0.939743
VEGFA	Model 1	G	rs735286	major	0.1110697	0.0135311	0.9346321	-2.50902	2.801575	0.8217802	0.939743
VEGFA	Model 1	A	rs735286	minor	-0.5604425	0.0235165	0.8111652	-5.039745	4.13015	0.8217802	0.939743
VEGFA	Model 1	C	rs833060	major	0.0576103	0.0135695	0.9661537	-2.568426	2.754426	0.9093754	0.939743
VEGFA	Model 1	A	rs833060	minor	-0.2824471	0.02349	0.9041815	-4.769328	4.415837	0.9093754	0.939743
PTGS1	Model 1	G	rs883484	major	-0.1278797	0.0130294	0.9217854	-2.646042	2.455417	0.9066174	0.939743
PTGS1	Model 1	A	rs883484	minor	0.2228551	0.0242424	0.926855	-4.42779	5.099805	0.9066174	0.939743
ALOX15	Model 1	G	rs9894225	major	-0.0591962	0.0124727	0.9621443	-2.472728	2.414064	0.9501846	0.939743
ALOX15	Model 1	A	rs9894225	minor	0.1240661	0.0245985	0.9598095	-4.588615	5.069522	0.9501846	0.939743
TLR4	Model 1	A	rs1927906	major	-0.0919091	0.0116698	0.9372122	-2.351115	2.219565	0.9765961	0.9489193
TLR4	Model 1	G	rs1927906	minor	0.0070795	0.030125	0.9981255	-5.726795	6.089699	0.9765961	0.9489193
ACE	Model 1	G	rs4295	major	-0.0701158	0.0144218	0.96122	-2.855212	2.794828	0.9722925	0.9489193
ACE	Model 1	C	rs4295	minor	0.0293772	0.0212385	0.9889684	-4.049048	4.281157	0.9722925	0.9489193
GRK4	Model 3	C	rs1008210	major	0.1952738	0.0148224	0.8953161	-2.673659	3.148776	0.7391261	0.9492417
GRK4	Model 3	A	rs1008210	minor	-0.7385995	0.0203463	0.7156652	-4.619058	3.299731	0.7391261	0.9492417
GRK4	Model 3	G	rs1024323	major	0.9221898	0.0148197	0.5357805	-1.967042	3.896573	0.3073555	0.9492417
GRK4	Model 3	A	rs1024323	minor	-1.818602	0.0193605	0.3433688	-5.47439	1.978573	0.3073555	0.9492417
ADRB2	Model 3	C	rs1042719	major	0.9755234	0.0147554	0.5107421	-1.902873	3.938378	0.302337	0.9492417
ADRB2	Model 3	G	rs1042719	minor	-1.896053	0.0202753	0.3453425	-5.718145	2.080983	0.302337	0.9492417
GRK4	Model 3	C	rs1056094	major	0.2969122	0.0137386	0.8291914	-2.36776	3.034311	0.6215436	0.9492417
GRK4	Model 3	G	rs1056094	minor	-1.068322	0.0214006	0.6158568	-5.132124	3.169559	0.6215436	0.9492417
PTGS2	Model 3	A	rs10911905	major	-0.400165	0.0114782	0.7269158	-2.615835	1.865916	0.5658812	0.9492417
PTGS2	Model 3	C	rs10911905	minor	1.976613	0.0375153	0.6019661	-5.252565	9.757374	0.5658812	0.9492417
PTGS1	Model 3	G	rs10985620	major	0.028551	0.0106377	0.9785962	-2.035399	2.135985	0.4985445	0.9492417
PTGS1	Model 3	C	rs10985620	minor	-4.592324	0.0681378	0.490391	-16.51964	9.03912	0.4985445	0.9492417
VEGFA	Model 3	C	rs1109324	major	-0.9009544	0.0115489	0.4334278	-3.118907	1.367776	0.1066082	0.9492417
VEGFA	Model 3	A	rs1109324	minor	5.805089	0.0368961	0.1264857	-1.576113	13.73984	0.1066082	0.9492417
ADRB2	Model 3	G	rs11168070	major	-0.6819118	0.0125134	0.5846308	-3.088144	1.784065	0.400371	0.9492417
ADRB2	Model 3	C	rs11168070	minor	1.931027	0.0259936	0.4620232	-3.131942	7.258621	0.400371	0.9492417
TLR4	Model 3	G	rs11536889	major	0.7183117	0.0116845	0.540307	-1.56204	3.051488	0.1189035	0.9492417
TLR4	Model 3	C	rs11536889	minor	-5.378886	0.0361171	0.126126	-11.84538	1.561945	0.1189035	0.9492417
PTGS1	Model 3	G	rs1213266	major	-0.7704611	0.0119743	0.5184793	-3.072182	1.585918	0.2864164	0.9492417
PTGS1	Model 3	A	rs1213266	minor	2.629869	0.0275871	0.3469445	-2.771947	8.331801	0.2864164	0.9492417
ADRB2	Model 3	G	rs12654778	major	-1.20413	0.0138676	0.3825597	-3.853235	1.517965	0.2321144	0.9492417
ADRB2	Model 3	A	rs12654778	minor	2.289905	0.0223913	0.3121937	-2.102129	6.878981	0.2321144	0.9492417
PTGS1	Model 3	A	rs1330344	major	0.4273699	0.0140563	0.7616535	-2.301629	3.232597	0.5368621	0.9492417
PTGS1	Model 3	G	rs1330344	minor	-1.275808	0.0209058	0.5392283	-5.239232	2.85339	0.5368621	0.9492417
VEGFA	Model 3	G	rs1413711	major	1.299773	0.0143959	0.3699049	-1.518496	4.198693	0.1564936	0.9492417
VEGFA	Model 3	A	rs1413711	minor	-2.743118	0.0213878	0.1937373	-6.735786	1.420477	0.1564936	0.9492417
GRK4	Model 3	A	rs1419046	major	0.2884423	0.01376	0.8342397	-2.380102	3.029935	0.6326311	0.9492417
GRK4	Model 3	T	rs1419046	minor	-1.031746	0.0213345	0.6269919	-5.084768	3.194345	0.6326311	0.9492417
EDN1	Model 3	G	rs1476046	major	-1.004569	0.0129771	0.4367389	-3.490727	1.545635	0.2500129	0.9492417
EDN1	Model 3	A	rs1476046	minor	2.69431	0.026182	0.3101366	-2.44259	8.101694	0.2500129	0.9492417
VEGFA	Model 3	T	rs1547651	major	-0.9588577	0.0115924	0.4060962	-3.183767	1.317181	0.0997747	0.9492417
VEGFA	Model 3	A	rs1547651	minor	5.788678	0.0362866	0.1212661	-1.47374	13.58641	0.0997747	0.9492417

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
TLR4	Model 3	A	rs1554973	major	0.0782466	0.0132932	0.9530922	-2.495544	2.719976	0.7648438	0.9492417
TLR4	Model 3	G	rs1554973	minor	-0.7166607	0.0210629	0.7328189	-4.731869	3.467774	0.7648438	0.9492417
EDN1	Model 3	G	rs1630736	major	1.884554	0.0145848	0.2008047	-0.9866565	4.839024	0.0545602	0.9492417
EDN1	Model 3	A	rs1630736	minor	-3.107603	0.0189185	0.0954927	-6.634542	0.5525689	0.0545602	0.9492417
ALOX15	Model 3	A	rs1871346	major	-0.0176974	0.0107155	0.9868252	-2.09563	2.104338	0.6672769	0.9492417
ALOX15	Model 3	G	rs1871346	minor	-2.564044	0.0581264	0.6550664	-13.05552	9.193427	0.6672769	0.9492417
PTGS1	Model 3	G	rs1888943	major	-0.6815021	0.010864	0.5291983	-2.77394	1.455968	0.0820756	0.9492417
PTGS1	Model 3	A	rs1888943	minor	8.319515	0.0477013	0.0941847	-1.348584	18.93511	0.0820756	0.9492417
TLR4	Model 3	G	rs1927907	major	0.2713448	0.0121966	0.8242235	-2.097207	2.697199	0.4952033	0.9492417
TLR4	Model 3	A	rs1927907	minor	-2.048176	0.0297087	0.4862291	-7.588833	3.82468	0.4952033	0.9492417
TLR4	Model 3	G	rs1927911	major	-0.6895034	0.0146615	0.637093	-3.50267	2.205675	0.5974358	0.9492417
TLR4	Model 3	A	rs1927911	minor	0.7481931	0.0197679	0.7061945	-3.080582	4.728223	0.5974358	0.9492417
TLR4	Model 3	A	rs1927914	major	-1.173142	0.0157487	0.4538434	-4.177028	1.924909	0.3731449	0.9492417
TLR4	Model 3	G	rs1927914	minor	1.130314	0.0174164	0.5188477	-2.263574	4.642056	0.3731449	0.9492417
GRK4	Model 3	G	rs2105380	major	-0.4076064	0.0105752	0.6994141	-2.450619	1.678193	0.1746875	0.9492417
GRK4	Model 3	A	rs2105380	minor	11.24608	0.0800183	0.1832051	-4.901642	30.13568	0.1746875	0.9492417
AGTR1	Model 3	G	rs2131127	major	-1.137322	0.0156131	0.463965	-4.116807	1.934748	0.3563422	0.9492417
AGTR1	Model 3	A	rs2131127	minor	1.354604	0.0184886	0.4669357	-2.252428	5.09474	0.3563422	0.9492417
AGT	Model 3	G	rs2148582	major	0.4031214	0.0135879	0.767231	-2.23551	3.112968	0.51776	0.9492417
AGT	Model 3	A	rs2148582	minor	-1.352947	0.0211602	0.519888	-5.360489	2.824297	0.51776	0.9492417
TLR4	Model 3	C	rs2149356	major	-1.11442	0.0155619	0.4716077	-4.08498	1.94814	0.3950823	0.9492417
TLR4	Model 3	A	rs2149356	minor	1.094117	0.0177003	0.5388419	-2.352895	4.66281	0.3950823	0.9492417
GRK4	Model 3	A	rs2185886	major	0.3606803	0.015224	0.8131018	-2.5897	3.400422	0.6199286	0.9492417
GRK4	Model 3	G	rs2185886	minor	-0.9337146	0.0182407	0.6071632	-4.412883	2.672088	0.6199286	0.9492417
PTGS2	Model 3	G	rs2206593	major	-0.0006661	0.0106738	0.9995022	-2.07094	2.113374	0.6379777	0.9492417
PTGS2	Model 3	A	rs2206593	minor	-3.513559	0.0740863	0.629355	-16.55431	11.56518	0.6379777	0.9492417
PTGS1	Model 3	G	rs2282169	major	0.4484915	0.0128161	0.7270417	-2.043257	3.003623	0.5165353	0.9492417
PTGS1	Model 3	C	rs2282169	minor	-1.424264	0.0238047	0.5469021	-5.9178	3.283892	0.5165353	0.9492417
AGTR1	Model 3	A	rs2320019	major	-0.4910784	0.0113264	0.6639185	-2.675765	1.742649	0.3309493	0.9492417
AGTR1	Model 3	G	rs2320019	minor	3.292906	0.0353233	0.3592601	-3.616383	10.69749	0.3309493	0.9492417
GRK4	Model 3	G	rs2471327	major	0.5987759	0.0149822	0.6903725	-2.312321	3.596624	0.4695304	0.9492417
GRK4	Model 3	A	rs2471327	minor	-1.33556	0.0190593	0.4806871	-4.953225	2.419799	0.4695304	0.9492417
GRK4	Model 3	A	rs2471337	major	0.2891213	0.013618	0.8321489	-2.352268	3.00196	0.5978432	0.9492417
GRK4	Model 3	G	rs2471337	minor	-1.196578	0.0220303	0.5848942	-5.371972	3.163052	0.5978432	0.9492417
GRK4	Model 3	A	rs2471347	major	0.4262681	0.0145645	0.7703061	-2.39996	3.334336	0.5638368	0.9492417
GRK4	Model 3	G	rs2471347	minor	-1.195114	0.020732	0.5620928	-5.129481	2.902415	0.5638368	0.9492417
GRK4	Model 3	A	rs2488806	major	0.3795406	0.0150416	0.8012089	-2.536549	3.382879	0.5913135	0.9492417
GRK4	Model 3	C	rs2488806	minor	-1.059371	0.0190299	0.575839	-4.681678	2.700593	0.5913135	0.9492417
GRK4	Model 3	A	rs2488813	major	0.6332616	0.0128742	0.6240066	-1.87425	3.20485	0.3030844	0.9492417
GRK4	Model 3	T	rs2488813	minor	-2.516865	0.0254438	0.3166607	-7.259019	2.467772	0.3030844	0.9492417
GRK4	Model 3	G	rs2488815	major	0.7293883	0.0149197	0.6262944	-2.173507	3.718424	0.3814836	0.9492417
GRK4	Model 3	A	rs2488815	minor	-1.61067	0.0191406	0.3964489	-5.233352	2.150497	0.3814836	0.9492417
AGTR1	Model 3	A	rs2638360	major	-0.7166744	0.0113595	0.5267637	-2.902709	1.518576	0.2045466	0.9492417
AGTR1	Model 3	G	rs2638360	minor	4.891163	0.0399791	0.2325854	-3.014094	13.44077	0.2045466	0.9492417
AGTR1	Model 3	G	rs2638363	major	-0.477368	0.0124903	0.7017217	-2.884147	1.989058	0.5737864	0.9492417
AGTR1	Model 3	A	rs2638363	minor	1.342642	0.02728	0.6250225	-3.933611	6.908681	0.5737864	0.9492417

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
TLR4	Model 3	A	rs2737191	major	0.0615288	0.0116839	0.9580253	-2.203845	2.379378	0.7676476	0.9492417
TLR4	Model 3	G	rs2737191	minor	-0.9932476	0.0321636	0.7563558	-7.041925	5.44901	0.7676476	0.9492417
AGTR1	Model 3	A	rs275645	major	-1.749388	0.0164136	0.2825229	-4.859815	1.462729	0.1875477	0.9492417
AGTR1	Model 3	G	rs275645	minor	1.742182	0.0172073	0.315744	-1.631932	5.232032	0.1875477	0.9492417
AGTR1	Model 3	G	rs275646	major	0.3834061	0.0110622	0.7294692	-1.769631	2.583634	0.2303295	0.9492417
AGTR1	Model 3	A	rs275646	minor	-5.644248	0.048797	0.2340921	-14.25036	3.825605	0.2303295	0.9492417
GRK4	Model 3	A	rs2798298	major	0.2431189	0.0149436	0.8709504	-2.65032	3.222557	0.7016849	0.9492417
GRK4	Model 3	G	rs2798298	minor	-0.8223941	0.0200072	0.6798795	-4.63622	3.143955	0.7016849	0.9492417
GRK4	Model 3	A	rs2857844	major	-0.9122231	0.0162042	0.5718355	-4.009771	2.285281	0.5133562	0.9492417
GRK4	Model 3	G	rs2857844	minor	0.7692564	0.0168438	0.6492424	-2.503149	4.151497	0.5133562	0.9492417
GRK4	Model 3	A	rs2960298	major	0.2771068	0.0135902	0.8386921	-2.358647	2.98401	0.6100338	0.9492417
GRK4	Model 3	G	rs2960298	minor	-1.158167	0.0220445	0.5973102	-5.337832	3.206046	0.6100338	0.9492417
GRK4	Model 3	C	rs2960306	major	0.1993298	0.013723	0.8846555	-2.459778	2.93093	0.7101582	0.9492417
GRK4	Model 3	A	rs2960306	minor	-0.8313497	0.0214699	0.6974814	-4.917809	3.430738	0.7101582	0.9492417
GRK4	Model 3	G	rs3021140	major	0.3485571	0.0135715	0.7977068	-2.285484	3.053602	0.5499091	0.9492417
GRK4	Model 3	A	rs3021140	minor	-1.32553	0.0219538	0.5434466	-5.481317	3.012978	0.5499091	0.9492417
VEGFA	Model 3	A	rs3025010	major	0.2414982	0.0144364	0.8673388	-2.555063	3.118318	0.7344543	0.9492417
VEGFA	Model 3	G	rs3025010	minor	-0.749323	0.021814	0.7303176	-4.903308	3.586115	0.7344543	0.9492417
VEGFA	Model 3	A	rs3025033	major	0.5245528	0.0121556	0.6669959	-1.842102	2.948269	0.3166299	0.9492417
VEGFA	Model 3	G	rs3025033	minor	-2.857488	0.0296605	0.3285922	-8.343707	2.957116	0.3166299	0.9492417
VEGFA	Model 3	G	rs3025035	major	0.4982577	0.0117304	0.6718746	-1.78596	2.835601	0.2253585	0.9492417
VEGFA	Model 3	A	rs3025035	minor	-3.815754	0.0323693	0.2296887	-9.728407	2.484168	0.2253585	0.9492417
EDN1	Model 3	A	rs3087459	major	-0.6519751	0.0124208	0.5985721	-3.041337	1.796268	0.4170345	0.9492417
EDN1	Model 3	C	rs3087459	minor	2.065403	0.0283371	0.470806	-3.448739	7.894464	0.4170345	0.9492417
AGTR1	Model 3	G	rs3772616	major	0.7793918	0.0136124	0.5685765	-1.873841	3.504365	0.3129489	0.9492417
AGTR1	Model 3	A	rs3772616	minor	-1.774956	0.0195898	0.3608322	-5.474844	2.069753	0.3129489	0.9492417
AGT	Model 3	G	rs3789670	major	-0.9110854	0.0119425	0.4436255	-3.203512	1.435633	0.1731643	0.9492417
AGT	Model 3	A	rs3789670	minor	4.101121	0.0319944	0.2093243	-2.226375	10.83811	0.1731643	0.9492417
AGT	Model 3	C	rs3789671	major	-1.191301	0.0141314	0.3965988	-3.890465	1.583666	0.265473	0.9492417
AGT	Model 3	A	rs3789671	minor	1.893301	0.0207577	0.3664415	-2.168959	6.124238	0.265473	0.9492417
PTGS1	Model 3	G	rs3842787	major	0.2102404	0.0108381	0.8463884	-1.896005	2.361706	0.2359973	0.9492417
PTGS1	Model 3	A	rs3842787	minor	-6.589812	0.0570082	0.232063	-16.46494	4.452709	0.2359973	0.9492417
AGTR1	Model 3	A	rs409742	major	0.1455104	0.0122161	0.9052781	-2.223814	2.572248	0.7177505	0.9492417
AGTR1	Model 3	G	rs409742	minor	-1.121179	0.0305264	0.7119404	-6.863657	4.975362	0.7177505	0.9492417
ACE	Model 3	C	rs4303	major	-0.3076848	0.0105261	0.7697676	-2.343335	1.770398	0.4236952	0.9492417
ACE	Model 3	A	rs4303	minor	7.469119	0.092562	0.436629	-10.36146	28.84649	0.4236952	0.9492417
ACE	Model 3	A	rs4316	major	-0.5875129	0.0167622	0.7252631	-3.800473	2.732757	0.7170238	0.9492417
ACE	Model 3	G	rs4316	minor	0.4105858	0.0177303	0.8172853	-3.018822	3.961263	0.7170238	0.9492417
ACE	Model 3	A	rs4351	major	-1.080355	0.0161348	0.5009612	-4.159611	2.097834	0.4364564	0.9492417
ACE	Model 3	G	rs4351	minor	1.066008	0.0183966	0.5644805	-2.513185	4.776609	0.4364564	0.9492417
ACE	Model 3	G	rs4353	major	-0.9681225	0.016716	0.5607116	-4.16011	2.330175	0.527974	0.9492417
ACE	Model 3	A	rs4353	minor	0.7285693	0.0172533	0.6740304	-2.620706	4.193039	0.527974	0.9492417
ACE	Model 3	G	rs4359	major	-0.8785538	0.0158842	0.5786486	-3.916913	2.255885	0.5446707	0.9492417
ACE	Model 3	A	rs4359	minor	0.7581748	0.0182173	0.6785133	-2.775947	4.420763	0.5446707	0.9492417
ACE	Model 3	G	rs4362	major	-0.9696712	0.0157398	0.5360111	-3.978054	2.132965	0.485602	0.9492417
ACE	Model 3	A	rs4362	minor	0.9125627	0.0183418	0.6205145	-2.650732	4.606286	0.485602	0.9492417

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ACE	Model 3	A	rs4363	major	-0.6664618	0.0157959	0.6721437	-3.694652	2.456945	0.6590483	0.9492417
ACE	Model 3	G	rs4363	minor	0.5237867	0.0182801	0.7751015	-3.01406	4.190687	0.6590483	0.9492417
ACE	Model 3	A	rs4459610	major	0.2781953	0.0159701	0.8619351	-2.811971	3.466616	0.7552794	0.9492417
ACE	Model 3	T	rs4459610	minor	-0.5622644	0.0180968	0.7554288	-4.027414	3.027997	0.7552794	0.9492417
AGTR1	Model 3	G	rs4488792	major	0.4941533	0.0131859	0.708606	-2.069735	3.125166	0.4535102	0.9492417
AGTR1	Model 3	A	rs4488792	minor	-1.521372	0.0215371	0.4767404	-5.591836	2.724592	0.4535102	0.9492417
PTGS2	Model 3	C	rs4648307	major	-0.6498468	0.0114197	0.5681866	-2.848824	1.598903	0.2804669	0.9492417
PTGS2	Model 3	A	rs4648307	minor	4.069849	0.0395324	0.3131722	-3.689232	12.45403	0.2804669	0.9492417
AGTR1	Model 3	G	rs4681443	major	-0.4996243	0.0125478	0.6898506	-2.916822	1.977757	0.5494159	0.9492417
AGTR1	Model 3	A	rs4681443	minor	1.157834	0.0230301	0.6172844	-3.306731	5.828539	0.5494159	0.9492417
TLR4	Model 3	G	rs4986791	major	-0.2967713	0.0106095	0.7794299	-2.348619	1.798189	0.4805526	0.9492417
TLR4	Model 3	A	rs4986791	minor	5.411758	0.0773168	0.4956101	-9.410701	22.65951	0.4805526	0.9492417
EDN1	Model 3	C	rs5370	major	-1.020967	0.0127995	0.4228805	-3.473118	1.493477	0.2244798	0.9492417
EDN1	Model 3	A	rs5370	minor	2.972543	0.0270761	0.2795812	-2.349548	8.584695	0.2244798	0.9492417
PTGS1	Model 3	C	rs5788	major	0.2548184	0.0124325	0.8378481	-2.1586	2.727768	0.609853	0.9492417
PTGS1	Model 3	A	rs5788	minor	-1.200331	0.0241073	0.6165352	-5.759995	3.579946	0.609853	0.9492417
VEGFB	Model 3	G	rs594942	major	0.2034763	0.0142273	0.8864192	-2.552092	3.036965	0.7558002	0.9492417
VEGFB	Model 3	A	rs594942	minor	-0.685903	0.0215559	0.7495712	-4.794405	3.599897	0.7558002	0.9492417
ALOX15	Model 3	G	rs6502804	major	1.465358	0.0168246	0.3874422	-1.825953	4.867012	0.2327591	0.9492417
ALOX15	Model 3	A	rs6502804	minor	-1.78555	0.0174131	0.301074	-5.080966	1.624277	0.2327591	0.9492417
GRK4	Model 3	A	rs6846128	major	-0.6152782	0.0107433	0.5657722	-2.686083	1.499592	0.0716546	0.9492417
GRK4	Model 3	G	rs6846128	minor	11.71455	0.0628697	0.0783744	-1.236838	26.36433	0.0716546	0.9492417
AGT	Model 3	G	rs699	major	0.6976869	0.0136442	0.6104676	-1.959501	3.426893	0.3411575	0.9492417
AGT	Model 3	A	rs699	minor	-1.870313	0.0209554	0.3678209	-5.819038	2.243971	0.3411575	0.9492417
VEGFA	Model 3	A	rs699946	major	0.8406485	0.0131788	0.5254357	-1.730714	3.479295	0.260561	0.9492417
VEGFA	Model 3	G	rs699946	minor	-2.602374	0.0249673	0.2911704	-7.253783	2.282313	0.260561	0.9492417
VEGFA	Model 3	C	rs699947	major	0.9020215	0.0142115	0.5276191	-1.869727	3.75206	0.3027112	0.9492417
VEGFA	Model 3	A	rs699947	minor	-2.03197	0.0215291	0.3405441	-6.079849	2.190368	0.3027112	0.9492417
AGTR1	Model 3	G	rs718858	major	-0.2452103	0.0116883	0.8336719	-2.504474	2.066407	0.7321874	0.9492417
AGTR1	Model 3	A	rs718858	minor	1.069095	0.0344417	0.757569	-5.528342	8.127265	0.7321874	0.9492417
ALOX15	Model 3	G	rs7217186	major	-1.96061	0.016117	0.2195227	-5.009144	1.18576	0.1275799	0.9492417
ALOX15	Model 3	A	rs7217186	minor	2.112267	0.017681	0.2374044	-1.36574	5.712914	0.1275799	0.9492417
ALOX15	Model 3	C	rs7220870	major	-1.40439	0.0122984	0.2504103	-3.752569	1.001078	0.0503243	0.9492417
ALOX15	Model 3	A	rs7220870	minor	5.65354	0.0304517	0.0712232	-0.4678193	12.15137	0.0503243	0.9492417
ALOX15	Model 3	A	rs743646	major	-0.4204768	0.0108304	0.6973172	-2.51199	1.715908	0.3925933	0.9492417
ALOX15	Model 3	G	rs743646	minor	4.863833	0.0581905	0.4146062	-6.439214	17.5324	0.3925933	0.9492417
ALOX15	Model 3	A	rs748694	major	0.6684439	0.0164778	0.6860694	-2.5308	3.972697	0.5248021	0.9492417
ALOX15	Model 3	G	rs748694	minor	-1.009354	0.0170929	0.552974	-4.270754	2.363158	0.5248021	0.9492417
AGT	Model 3	A	rs7536290	major	0.1565104	0.0130183	0.904405	-2.366699	2.744929	0.7059078	0.9492417
AGT	Model 3	G	rs7536290	minor	-1.00931	0.025336	0.6889523	-5.804905	4.030435	0.7059078	0.9492417
AGT	Model 3	G	rs7549009	major	-0.7015717	0.0133957	0.5993004	-3.274733	1.940043	0.4826102	0.9492417
AGT	Model 3	A	rs7549009	minor	1.321537	0.0227188	0.5634728	-3.091131	5.935134	0.4826102	0.9492417
TLR4	Model 3	C	rs7873784	major	0.0732269	0.0117083	0.9501614	-2.197089	2.396244	0.6888012	0.9492417
TLR4	Model 3	G	rs7873784	minor	-1.457114	0.0346023	0.6715101	-7.918629	5.457817	0.6888012	0.9492417
ACE	Model 3	A	rs8066276	major	0.961048	0.0155561	0.538797	-2.070731	4.086688	0.3521156	0.9492417
ACE	Model 3	G	rs8066276	minor	-1.59775	0.0190291	0.3975269	-5.200193	2.141587	0.3521156	0.9492417

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
VEGFA	Model 3	A	rs833069	major	-0.5705404	0.0157301	0.7161251	-3.589215	2.54265	0.7551425	0.9492417
VEGFA	Model 3	G	rs833069	minor	0.2735995	0.0184902	0.8825558	-3.29527	3.974177	0.7551425	0.9492417
PTGS1	Model 3	G	rs876567	major	0.162364	0.0105465	0.8777788	-1.886825	2.254352	0.1426993	0.9492417
PTGS1	Model 3	A	rs876567	minor	-11.17035	0.0803986	0.1409906	-24.12083	3.990417	0.1426993	0.9492417
ALOX15	Model 3	A	rs916055	major	1.149132	0.0139828	0.4140484	-1.585301	3.959541	0.1708427	0.9492417
ALOX15	Model 3	G	rs916055	minor	-2.817387	0.022328	0.2008659	-6.978583	1.529956	0.1708427	0.9492417
AGT	Model 3	G	rs943580	major	0.7861122	0.013569	0.5640164	-1.858942	3.502455	0.297557	0.9492417
AGT	Model 3	A	rs943580	minor	-2.057123	0.0213535	0.3305846	-6.071647	2.128983	0.297557	0.9492417
GRK4	Model 2	G	rs1024323	major	1.007516	0.0148503	0.4997984	-1.890042	3.990649	0.277888	0.951433
GRK4	Model 2	A	rs1024323	minor	-1.911276	0.0193982	0.3200635	-5.570581	1.889834	0.277888	0.951433
ADRB2	Model 2	C	rs1042719	major	1.004771	0.0147704	0.4986523	-1.877346	3.971542	0.2978653	0.951433
ADRB2	Model 2	G	rs1042719	minor	-1.89649	0.0203056	0.3459494	-5.724165	2.086593	0.2978653	0.951433
GRK4	Model 2	C	rs1056094	major	0.2934791	0.0137673	0.8314808	-2.3766	3.036587	0.6370465	0.951433
GRK4	Model 2	G	rs1056094	minor	-1.014067	0.0214392	0.6345974	-5.087278	3.233948	0.6370465	0.951433
PTGS2	Model 2	A	rs10911905	major	-0.3928502	0.0115024	0.7322647	-2.613299	1.878225	0.554991	0.951433
PTGS2	Model 2	C	rs10911905	minor	2.057108	0.0375952	0.5882009	-5.192624	9.861212	0.554991	0.951433
PTGS1	Model 2	G	rs10985620	major	0.0418139	0.0106628	0.9687336	-2.027241	2.154564	0.5210673	0.951433
PTGS1	Model 2	C	rs10985620	minor	-4.354817	0.0682854	0.5145254	-16.33603	9.34219	0.5210673	0.951433
VEGFA	Model 2	C	rs1109324	major	-0.9085639	0.0115728	0.4304898	-3.130882	1.364738	0.0969054	0.951433
VEGFA	Model 2	A	rs1109324	minor	6.003768	0.0369303	0.1147053	-1.39789	13.96104	0.0969054	0.951433
ADRB2	Model 2	G	rs11168070	major	-0.7651693	0.0125269	0.5399039	-3.171944	1.701429	0.3225846	0.951433
ADRB2	Model 2	C	rs11168070	minor	2.311019	0.0259871	0.3795192	-2.769591	7.657107	0.3225846	0.951433
TLR4	Model 2	G	rs11536889	major	0.7025635	0.0116993	0.5496977	-1.580297	3.038375	0.1403227	0.951433
TLR4	Model 2	C	rs11536889	minor	-5.074325	0.0361447	0.1499654	-11.56641	1.894355	0.1403227	0.951433
PTGS1	Model 2	G	rs1213266	major	-0.7196068	0.0119995	0.5473995	-3.027293	1.642996	0.3118636	0.951433
PTGS1	Model 2	A	rs1213266	minor	2.507801	0.0276131	0.3699403	-2.892543	8.208468	0.3118636	0.951433
ADRB2	Model 2	G	rs12654778	major	-1.137001	0.0138914	0.4106025	-3.792403	1.591691	0.2542217	0.951433
ADRB2	Model 2	A	rs12654778	minor	2.199761	0.0224157	0.3319282	-2.19308	6.789901	0.2542217	0.951433
PTGS1	Model 2	A	rs1330344	major	0.4777123	0.0140834	0.7351361	-2.257833	3.289818	0.5168799	0.951433
PTGS1	Model 2	G	rs1330344	minor	-1.31179	0.0209294	0.5282398	-5.278159	2.820666	0.5168799	0.951433
VEGFA	Model 2	G	rs1413711	major	1.395198	0.0144217	0.3369159	-1.430713	4.302125	0.1364421	0.951433
VEGFA	Model 2	A	rs1413711	minor	-2.861479	0.0214316	0.1758401	-6.857292	1.305755	0.1364421	0.951433
GRK4	Model 2	A	rs1419046	major	0.3121068	0.0137879	0.8212395	-2.362404	3.059878	0.6268709	0.951433
GRK4	Model 2	T	rs1419046	minor	-1.032959	0.0213726	0.6271998	-5.09302	3.200789	0.6268709	0.951433
EDN1	Model 2	G	rs1476046	major	-0.9309623	0.0130031	0.4721191	-3.423891	1.626317	0.2827834	0.951433
EDN1	Model 2	A	rs1476046	minor	2.525581	0.0262144	0.3415969	-2.609066	7.930937	0.2827834	0.951433
VEGFA	Model 2	T	rs1547651	major	-0.968086	0.0116151	0.4024933	-3.197094	1.312248	0.0894393	0.951433
VEGFA	Model 2	A	rs1547651	minor	6.006903	0.0363127	0.1084944	-1.27555	13.82655	0.0894393	0.951433
EDN1	Model 2	G	rs1630736	major	1.768057	0.0145935	0.2300533	-1.101543	4.720921	0.0728468	0.951433
EDN1	Model 2	A	rs1630736	minor	-2.891454	0.0189365	0.1215951	-6.429559	0.7804345	0.0728468	0.951433
ALOX15	Model 2	A	rs1871346	major	0.0315734	0.010736	0.976548	-2.051312	2.158752	0.5852702	0.951433
ALOX15	Model 2	G	rs1871346	minor	-3.189221	0.0580911	0.5770047	-13.60741	8.485313	0.5852702	0.951433
PTGS1	Model 2	G	rs1888943	major	-0.6555149	0.0108888	0.5459868	-2.753223	1.487443	0.0832306	0.951433
PTGS1	Model 2	A	rs1888943	minor	8.334439	0.0478089	0.09436	-1.355806	18.9766	0.0832306	0.951433
TLR4	Model 2	G	rs1927907	major	0.3602906	0.0122158	0.7685071	-2.014049	2.792164	0.4363254	0.951433
TLR4	Model 2	A	rs1927907	minor	-2.287319	0.0297378	0.4366976	-7.819713	3.577113	0.4363254	0.951433

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
TLR4	Model 2	A	rs1927914	major	-0.9480377	0.0157591	0.5456811	-3.960714	2.159144	0.4697916	0.951433
TLR4	Model 2	G	rs1927914	minor	0.9206491	0.0174191	0.5989281	-2.466707	4.425648	0.4697916	0.951433
GRK4	Model 2	G	rs2105380	major	-0.3752548	0.010598	0.7228542	-2.423285	1.715761	0.2132119	0.951433
GRK4	Model 2	A	rs2105380	minor	10.27876	0.080116	0.2222826	-5.746609	29.02882	0.2132119	0.951433
AGTR1	Model 2	G	rs2131127	major	-1.035528	0.0156364	0.505753	-4.022475	2.044376	0.3989655	0.951433
AGTR1	Model 2	A	rs2131127	minor	1.245331	0.0185129	0.5039511	-2.362471	4.986445	0.3989655	0.951433
AGT	Model 2	G	rs2148582	major	0.453856	0.0136149	0.7395068	-2.191271	3.170517	0.4975566	0.951433
AGT	Model 2	A	rs2148582	minor	-1.392072	0.0212081	0.5087663	-5.406903	2.793161	0.4975566	0.951433
TLR4	Model 2	C	rs2149356	major	-0.8913431	0.0155728	0.5654619	-3.870645	2.180295	0.4962621	0.951433
TLR4	Model 2	A	rs2149356	minor	0.8746296	0.0177015	0.6228633	-2.565138	4.435833	0.4962621	0.951433
GRK4	Model 2	A	rs2185886	major	0.3549411	0.0152578	0.8164167	-2.601718	3.401353	0.6330045	0.951433
GRK4	Model 2	G	rs2185886	minor	-0.8942792	0.0182808	0.6232581	-4.382347	2.721031	0.6330045	0.951433
PTGS1	Model 2	G	rs2282169	major	0.5311157	0.0128398	0.6800215	-1.967228	3.093129	0.4624704	0.951433
PTGS1	Model 2	C	rs2282169	minor	-1.590295	0.02382	0.501106	-6.079089	3.113033	0.4624704	0.951433
AGTR1	Model 2	A	rs2320019	major	-0.4649503	0.0113483	0.6814077	-2.654403	1.773747	0.3395228	0.951433
AGTR1	Model 2	G	rs2320019	minor	3.259261	0.0353899	0.3650124	-3.660342	10.67587	0.3395228	0.951433
GRK4	Model 2	G	rs2471327	major	0.6237788	0.0150151	0.6788583	-2.294341	3.629052	0.4647073	0.951433
GRK4	Model 2	A	rs2471327	minor	-1.336052	0.0190999	0.4814595	-4.961275	2.427455	0.4647073	0.951433
GRK4	Model 2	A	rs2471337	major	0.2808092	0.0136451	0.8372188	-2.365554	2.998901	0.6165588	0.951433
GRK4	Model 2	G	rs2471337	minor	-1.132393	0.0220711	0.6059737	-5.318077	3.238332	0.6165588	0.951433
GRK4	Model 2	A	rs2471347	major	0.383506	0.014593	0.7931457	-2.446971	3.296109	0.602779	0.951433
GRK4	Model 2	G	rs2471347	minor	-1.08162	0.0207725	0.600719	-5.02804	3.028789	0.602779	0.951433
GRK4	Model 2	A	rs2488806	major	0.3968107	0.0150747	0.7928292	-2.526105	3.407375	0.5904462	0.951433
GRK4	Model 2	C	rs2488806	minor	-1.048851	0.0190719	0.5804905	-4.679398	2.719974	0.5904462	0.951433
GRK4	Model 2	A	rs2488813	major	0.5896838	0.0129035	0.6487382	-1.922366	3.166075	0.340934	0.951433
GRK4	Model 2	T	rs2488813	minor	-2.330625	0.0254874	0.3550622	-7.089787	2.672317	0.340934	0.951433
GRK4	Model 2	G	rs2488815	major	0.7308356	0.014951	0.6263353	-2.178097	3.726271	0.3890048	0.951433
GRK4	Model 2	A	rs2488815	minor	-1.578017	0.0191847	0.4072472	-5.210102	2.193238	0.3890048	0.951433
AGTR1	Model 2	A	rs2638360	major	-0.7573916	0.0113805	0.5042543	-2.94652	1.481115	0.1634543	0.951433
AGTR1	Model 2	G	rs2638360	minor	5.423249	0.0400175	0.1872222	-2.529449	14.02481	0.1634543	0.951433
AGTR1	Model 2	G	rs2638363	major	-0.49176	0.0125143	0.6937187	-2.902769	1.979116	0.5386987	0.951433
AGTR1	Model 2	A	rs2638363	minor	1.501171	0.0273103	0.5854714	-3.789051	7.082281	0.5386987	0.951433
AGTR1	Model 2	A	rs275645	major	-1.757512	0.0164409	0.2810736	-4.872768	1.459764	0.1815329	0.951433
AGTR1	Model 2	G	rs275645	minor	1.786647	0.0172269	0.3042119	-1.592709	5.282053	0.1815329	0.951433
AGTR1	Model 2	G	rs275646	major	0.4118552	0.0110849	0.7108777	-1.746165	2.617274	0.2218519	0.951433
AGTR1	Model 2	A	rs275646	minor	-5.735659	0.0488813	0.2271869	-14.34758	3.742149	0.2218519	0.951433
GRK4	Model 2	A	rs2857844	major	-0.8308233	0.0162299	0.6073329	-3.935753	2.374462	0.5511675	0.951433
GRK4	Model 2	G	rs2857844	minor	0.7039216	0.0168642	0.6775413	-2.570264	4.088139	0.5511675	0.951433
GRK4	Model 2	A	rs2960298	major	0.2784673	0.0136175	0.8382326	-2.362546	2.990918	0.6213126	0.951433
GRK4	Model 2	G	rs2960298	minor	-1.114499	0.0220856	0.6119447	-5.303639	3.259958	0.6213126	0.951433
GRK4	Model 2	G	rs3021140	major	0.3367458	0.0135987	0.8047924	-2.302197	3.046969	0.5712397	0.951433
GRK4	Model 2	A	rs3021140	minor	-1.252056	0.0219958	0.566897	-5.41872	3.098166	0.5712397	0.951433
VEGFA	Model 2	A	rs3025033	major	0.4907004	0.0121819	0.6878976	-1.880203	2.918892	0.3596258	0.951433
VEGFA	Model 2	G	rs3025033	minor	-2.612536	0.0297192	0.3732723	-8.123163	3.22861	0.3596258	0.951433
VEGFA	Model 2	G	rs3025035	major	0.5294781	0.0117536	0.6533173	-1.759908	2.872216	0.2203265	0.951433
VEGFA	Model 2	A	rs3025035	minor	-3.83797	0.032415	0.2275904	-9.757323	2.469656	0.2203265	0.951433

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
EDN1	Model 2	A	rs3087459	major	-0.5397831	0.0124435	0.6636844	-2.936162	1.915759	0.5019169	0.951433
EDN1	Model 2	C	rs3087459	minor	1.707983	0.0283688	0.5506557	-3.792814	7.523295	0.5019169	0.951433
AGTR1	Model 2	G	rs3772616	major	0.8429319	0.013637	0.538345	-1.816701	3.57461	0.2890987	0.951433
AGTR1	Model 2	A	rs3772616	minor	-1.844987	0.0196244	0.3428865	-5.548656	2.003912	0.2890987	0.951433
AGT	Model 2	G	rs3789670	major	-0.8846239	0.0119641	0.4578435	-3.181754	1.467009	0.1822966	0.951433
AGT	Model 2	A	rs3789670	minor	4.030565	0.0320522	0.217933	-2.303701	10.77552	0.1822966	0.951433
AGT	Model 2	C	rs3789671	major	-1.218771	0.014156	0.3865635	-3.921812	1.560317	0.2458882	0.951433
AGT	Model 2	A	rs3789671	minor	2.00295	0.0207986	0.3405658	-2.07154	6.246967	0.2458882	0.951433
PTGS1	Model 2	G	rs3842787	major	0.2397598	0.0108605	0.8255274	-1.87141	2.39635	0.2229335	0.951433
PTGS1	Model 2	A	rs3842787	minor	-6.7579	0.0570868	0.2206038	-16.62811	4.280818	0.2229335	0.951433
ACE	Model 2	C	rs4303	major	-0.3069731	0.0105476	0.7707425	-2.346766	1.775427	0.3759301	0.951433
ACE	Model 2	A	rs4303	minor	8.311256	0.0923176	0.3873437	-9.615759	29.79396	0.3759301	0.951433
ACE	Model 2	A	rs4351	major	-0.9399117	0.0161589	0.5590709	-4.028072	2.247619	0.4973843	0.951433
ACE	Model 2	G	rs4351	minor	0.9340205	0.0184256	0.6139774	-2.646023	4.645714	0.4973843	0.951433
ACE	Model 2	G	rs4353	major	-0.8574141	0.0167444	0.6071777	-4.058299	2.450261	0.5754371	0.951433
ACE	Model 2	A	rs4353	minor	0.6503782	0.0172791	0.7076089	-2.701221	4.117428	0.5754371	0.951433
ACE	Model 2	G	rs4359	major	-0.7549598	0.0159125	0.6340044	-3.802437	2.389059	0.6039196	0.951433
ACE	Model 2	A	rs4359	minor	0.6486176	0.0182449	0.723145	-2.886914	4.312866	0.6039196	0.951433
ACE	Model 2	G	rs4362	major	-0.8843663	0.0157657	0.5732634	-3.900228	2.226141	0.5221562	0.951433
ACE	Model 2	A	rs4362	minor	0.8454215	0.0183694	0.6468369	-2.720764	4.542341	0.5221562	0.951433
ACE	Model 2	A	rs4459610	major	0.5574997	0.0159797	0.7279811	-2.543124	3.756771	0.5996311	0.951433
ACE	Model 2	T	rs4459610	minor	-0.8572429	0.018104	0.6344982	-4.313463	2.723817	0.5996311	0.951433
AGTR1	Model 2	G	rs4488792	major	0.5486466	0.01321	0.678822	-2.021251	3.18595	0.4259414	0.951433
AGTR1	Model 2	A	rs4488792	minor	-1.594925	0.0215696	0.4562106	-5.668354	2.654403	0.4259414	0.951433
PTGS2	Model 2	C	rs4648307	major	-0.6649031	0.011442	0.5599933	-2.867792	1.587946	0.2524278	0.951433
PTGS2	Model 2	A	rs4648307	minor	4.355966	0.0396064	0.2819484	-3.438438	12.77953	0.2524278	0.951433
AGTR1	Model 2	G	rs4681443	major	-0.4262338	0.0125714	0.7340966	-2.849693	2.05768	0.6070092	0.951433
AGTR1	Model 2	A	rs4681443	minor	0.9989127	0.0230593	0.6665301	-3.464164	5.668327	0.6070092	0.951433
TLR4	Model 2	G	rs4986791	major	-0.2622877	0.0106252	0.804821	-2.317851	1.836531	0.4797066	0.951433
TLR4	Model 2	A	rs4986791	minor	5.46536	0.0773995	0.4919258	-9.379335	22.74179	0.4797066	0.951433
EDN1	Model 2	C	rs5370	major	-0.9592305	0.0128237	0.4524542	-3.417498	1.561607	0.249713	0.951433
EDN1	Model 2	A	rs5370	minor	2.82728	0.0271041	0.3038949	-2.492654	8.437466	0.249713	0.951433
PTGS1	Model 2	C	rs5788	major	0.3900301	0.0124535	0.7546644	-2.03066	2.870533	0.494448	0.951433
PTGS1	Model 2	A	rs5788	minor	-1.556741	0.0241211	0.5155446	-6.102501	3.209088	0.494448	0.951433
ALOX15	Model 2	G	rs6502804	major	1.472197	0.0168478	0.3859046	-1.823815	4.878864	0.2360623	0.951433
ALOX15	Model 2	A	rs6502804	minor	-1.759435	0.0174363	0.3089029	-5.060042	1.655919	0.2360623	0.951433
GRK4	Model 2	A	rs6846128	major	-0.5425451	0.010766	0.6134508	-2.619217	1.578412	0.1136748	0.951433
GRK4	Model 2	G	rs6846128	minor	10.20901	0.0628564	0.1222968	-2.565299	24.65812	0.1136748	0.951433
AGT	Model 2	G	rs699	major	0.713753	0.0136728	0.6030594	-1.949343	3.44918	0.34597	0.951433
AGT	Model 2	A	rs699	minor	-1.83524	0.0210032	0.3780395	-5.794202	2.290097	0.34597	0.951433
VEGFA	Model 2	A	rs699946	major	0.8037334	0.0132024	0.5444242	-1.771231	3.446198	0.2912039	0.951433
VEGFA	Model 2	G	rs699946	minor	-2.433614	0.0250116	0.3248479	-7.101151	2.468435	0.2912039	0.951433
VEGFA	Model 2	C	rs699947	major	0.8995913	0.0142418	0.5296021	-1.877906	3.75571	0.312915	0.951433
VEGFA	Model 2	A	rs699947	minor	-1.979949	0.0215726	0.3541428	-6.037992	2.253352	0.312915	0.951433
ALOX15	Model 2	G	rs7217186	major	-1.984587	0.0161365	0.2144391	-5.036008	1.164885	0.1196998	0.951433
ALOX15	Model 2	A	rs7217186	minor	2.180048	0.0177098	0.2236041	-1.305833	5.78905	0.1196998	0.951433

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ALOX15	Model 2	C	rs7220870	major	-1.401298	0.0123055	0.2517346	-3.750887	1.005648	0.0463673	0.951433
ALOX15	Model 2	A	rs7220870	minor	5.777031	0.0304315	0.0652518	-0.3475347	12.27801	0.0463673	0.951433
ALOX15	Model 2	A	rs743646	major	-0.4115479	0.0108512	0.7039903	-2.507221	1.729173	0.374869	0.951433
ALOX15	Model 2	G	rs743646	minor	5.085337	0.0582596	0.3947482	-6.254279	17.79661	0.374869	0.951433
ALOX15	Model 2	A	rs748694	major	0.6514825	0.0164847	0.6937226	-2.548537	3.956582	0.5425576	0.951433
ALOX15	Model 2	G	rs748694	minor	-0.9529966	0.0170817	0.5752094	-4.214147	2.419183	0.5425576	0.951433
AGT	Model 2	G	rs7549009	major	-0.721133	0.01342	0.5897983	-3.298399	1.924822	0.4540379	0.951433
AGT	Model 2	A	rs7549009	minor	1.440735	0.0227566	0.5297614	-2.984314	6.067619	0.4540379	0.951433
ACE	Model 2	A	rs8066276	major	1.112746	0.0155776	0.4776346	-1.927722	4.247476	0.2968155	0.951433
ACE	Model 2	G	rs8066276	minor	-1.759663	0.0190616	0.3518938	-5.362207	1.980017	0.2968155	0.951433
PTGS1	Model 2	G	rs876567	major	0.1665235	0.0105709	0.8749624	-1.887439	2.263485	0.1567658	0.951433
PTGS1	Model 2	A	rs876567	minor	-10.82205	0.0805458	0.1553379	-23.84529	4.428301	0.1567658	0.951433
ALOX15	Model 2	A	rs916055	major	1.131592	0.0140004	0.4217526	-1.605767	3.945106	0.1818297	0.951433
ALOX15	Model 2	G	rs916055	minor	-2.738401	0.0223483	0.2143746	-6.90669	1.616524	0.1818297	0.951433
AGT	Model 2	G	rs943580	major	0.7741374	0.0135941	0.5706578	-1.875438	3.495258	0.3163012	0.951433
AGT	Model 2	A	rs943580	minor	-1.96755	0.0213992	0.3533128	-5.994162	2.231537	0.3163012	0.951433
ACE	Model 1	G	rs4311	major	-0.0427216	0.0145795	0.9766242	-2.858607	2.854789	0.9952168	0.9586035
ACE	Model 1	A	rs4311	minor	-0.0599489	0.0211295	0.9773642	-4.114247	4.165775	0.9952168	0.9586035
ADRB2	Model 2	G	rs1042713	major	0.3961263	0.0160846	0.8058948	-2.71951	3.611549	0.6945869	0.9623794
ADRB2	Model 2	A	rs1042713	minor	-0.6526477	0.0177872	0.7128603	-4.056448	2.871909	0.6945869	0.9623794
TLR4	Model 2	G	rs1927911	major	-0.5498387	0.014678	0.7072689	-3.370096	2.352731	0.6760424	0.9623794
TLR4	Model 2	A	rs1927911	minor	0.5874743	0.0197687	0.7670596	-3.235348	4.561323	0.6760424	0.9623794
ACE	Model 2	A	rs4363	major	-0.6055534	0.0158216	0.7011324	-3.640447	2.524926	0.6854383	0.9623794
ACE	Model 2	G	rs4363	minor	0.4884216	0.0183053	0.7901632	-3.052968	4.159175	0.6854383	0.9623794
AGT	Model 2	A	rs7536290	major	0.2256333	0.0130437	0.8628535	-2.30418	2.820956	0.6629468	0.9623794
AGT	Model 2	G	rs7536290	minor	-1.123133	0.025383	0.6564314	-5.921868	3.920375	0.6629468	0.9623794
TLR4	Model 2	C	rs7873784	major	0.1150165	0.0117266	0.9219322	-2.159765	2.442687	0.6700089	0.9623794
TLR4	Model 2	G	rs7873784	minor	-1.51555	0.034656	0.6595547	-7.982927	5.406384	0.6700089	0.9623794
VEGFA	Model 2	A	rs833069	major	-0.6372519	0.015761	0.6851128	-3.659751	2.480072	0.6938509	0.9623794
VEGFA	Model 2	G	rs833069	minor	0.4307147	0.0185259	0.8165902	-3.150523	4.144378	0.6938509	0.9623794
GRK4	Model 2	C	rs2960306	major	0.2194751	0.0137505	0.8733566	-2.44542	2.957167	0.7070884	0.9680377
GRK4	Model 2	A	rs2960306	minor	-0.82472	0.0215113	0.7003345	-4.919157	3.446034	0.7070884	0.9680377
TLR4	Model 2	A	rs1554973	major	0.1642706	0.0133129	0.9019018	-2.415497	2.812238	0.7155627	0.9681142
TLR4	Model 2	G	rs1554973	minor	-0.8050658	0.0210881	0.7015728	-4.821405	3.380755	0.7155627	0.9681142
GRK4	Model 2	A	rs2798298	major	0.1917552	0.0149706	0.8982022	-2.705341	3.175117	0.7465591	0.9686446
GRK4	Model 2	G	rs2798298	minor	-0.7088069	0.0200404	0.7227029	-4.533206	3.268798	0.7465591	0.9686446
VEGFA	Model 2	A	rs3025010	major	0.2452577	0.0144687	0.8655939	-2.557584	3.12872	0.7466403	0.9686446
VEGFA	Model 2	G	rs3025010	minor	-0.7004063	0.0218492	0.7477536	-4.863011	3.644328	0.7466403	0.9686446
AGTR1	Model 2	A	rs422858	major	-0.2785108	0.0121774	0.8188919	-2.630407	2.130194	0.7385545	0.9686446
AGTR1	Model 2	C	rs422858	minor	0.9258302	0.0313435	0.7688018	-5.087663	7.320328	0.7385545	0.9686446
VEGFB	Model 2	G	rs594942	major	0.2384844	0.0142452	0.8672352	-2.521475	3.076587	0.7496467	0.9686446
VEGFB	Model 2	A	rs594942	minor	-0.6752435	0.0215864	0.7536857	-4.789882	3.617214	0.7496467	0.9686446
GRK4	Model 2	C	rs1008210	major	0.1544313	0.014849	0.917253	-2.718407	3.112108	0.7768502	0.9737254
GRK4	Model 2	A	rs1008210	minor	-0.6418526	0.0203824	0.7521295	-4.532856	3.407739	0.7768502	0.9737254
AGT	Model 2	A	rs1326886	major	-0.3161973	0.012957	0.8069538	-2.815819	2.247715	0.7670289	0.9737254
AGT	Model 2	G	rs1326886	minor	0.572089	0.024497	0.8159107	-4.142605	5.518672	0.7670289	0.9737254

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ACE	Model 2	G	rs4309	major	-0.4278681	0.016241	0.7918226	-3.547502	2.792666	0.7799771	0.9737254
ACE	Model 2	A	rs4309	minor	0.3243461	0.0178061	0.8557297	-3.116512	3.887408	0.7799771	0.9737254
ACE	Model 2	A	rs4316	major	-0.4468755	0.0167903	0.7897192	-3.669695	2.883766	0.7874475	0.9737254
ACE	Model 2	G	rs4316	minor	0.2965912	0.0177547	0.8675594	-3.133556	3.848204	0.7874475	0.9737254
ADRB2	Model 3	G	rs1042713	major	0.2014974	0.0160798	0.9004024	-2.907189	3.409717	0.8025913	0.9818936
ADRB2	Model 3	A	rs1042713	minor	-0.4669351	0.0177897	0.7925361	-3.87757	3.064716	0.8025913	0.9818936
PTGS2	Model 2	G	rs2206593	major	-0.0530558	0.0106932	0.9604275	-2.125975	2.063766	0.8321224	0.9864613
PTGS2	Model 2	A	rs2206593	minor	-1.647983	0.0739777	0.8223181	-14.92277	13.6981	0.8321224	0.9864613
ALOX15	Model 2	A	rs2255888	major	-0.2062106	0.0128057	0.8719708	-2.679728	2.330174	0.8492145	0.9864613
ALOX15	Model 2	G	rs2255888	minor	0.3284292	0.0230855	0.8870826	-4.109944	4.972237	0.8492145	0.9864613
TLR4	Model 2	A	rs2737191	major	0.0389703	0.0117043	0.9734505	-2.229793	2.360381	0.8465657	0.9864613
TLR4	Model 2	G	rs2737191	minor	-0.653928	0.0322061	0.8386205	-6.73111	5.819229	0.8465657	0.9864613
AGTR1	Model 2	A	rs409742	major	0.0838642	0.0122384	0.9454041	-2.288271	2.513587	0.8115312	0.9864613
AGTR1	Model 2	G	rs409742	minor	-0.7533083	0.0305372	0.8044798	-6.519131	5.368146	0.8115312	0.9864613
AGTR1	Model 2	G	rs718858	major	-0.1451288	0.0117016	0.9012494	-2.409211	2.17148	0.8432001	0.9864613
AGTR1	Model 2	A	rs718858	minor	0.6121311	0.0344054	0.8592502	-5.948792	7.630738	0.8432001	0.9864613
ALOX15	Model 2	G	rs9894225	major	0.0504827	0.0125131	0.9678352	-2.373439	2.534587	0.8462644	0.9864613
ALOX15	Model 2	A	rs9894225	minor	-0.5179889	0.024694	0.8334698	-5.218186	4.415289	0.8462644	0.9864613
PTGS1	Model 3	G	rs10306202	major	-0.1105798	0.0118026	0.9253323	-2.39477	2.227066	0.9718793	0.9869372
PTGS1	Model 3	A	rs10306202	minor	-0.2325694	0.0307909	0.9397367	-6.075361	5.973687	0.9718793	0.9869372
ALOX15	Model 3	A	rs1076039	major	-0.14296	0.0110516	0.8970278	-2.282671	2.043605	0.9336132	0.9869372
ALOX15	Model 3	T	rs1076039	minor	0.2803995	0.0479866	0.9534807	-8.721228	10.16974	0.9336132	0.9869372
AGT	Model 3	A	rs1326886	major	-0.2471516	0.0129329	0.8482985	-2.743912	2.313705	0.8546349	0.9869372
AGT	Model 3	G	rs1326886	minor	0.3008096	0.0244612	0.9022983	-4.394461	5.226669	0.8546349	0.9869372
GRK4	Model 3	G	rs1801058	major	0.0006996	0.0147038	0.9996205	-2.840089	2.924548	0.8703792	0.9869372
GRK4	Model 3	A	rs1801058	minor	-0.4562861	0.0204492	0.8230817	-4.367076	3.614431	0.8703792	0.9869372
TLR4	Model 3	A	rs1927906	major	-0.1310387	0.0116957	0.9107562	-2.394315	2.184718	0.9543396	0.9869372
TLR4	Model 3	G	rs1927906	minor	-0.3240358	0.0302022	0.9144434	-6.053144	5.754448	0.9543396	0.9869372
ALOX15	Model 3	A	rs2255888	major	-0.2159125	0.0127878	0.865811	-2.68578	2.316641	0.8590046	0.9869372
ALOX15	Model 3	G	rs2255888	minor	0.2843274	0.023116	0.9022698	-4.157814	4.932355	0.8590046	0.9869372
AGT	Model 3	G	rs2478545	major	-0.1680315	0.0136978	0.9023114	-2.81259	2.548488	0.9566368	0.9869372
AGT	Model 3	A	rs2478545	minor	-0.0159899	0.0216419	0.9941059	-4.168352	4.316293	0.9566368	0.9869372
AGTR1	Model 3	A	rs422858	major	-0.2101804	0.0121575	0.8626367	-2.559889	2.19619	0.8414623	0.9869372
AGTR1	Model 3	C	rs422858	minor	0.5105663	0.0313524	0.8709977	-5.479833	6.880619	0.8414623	0.9869372
ACE	Model 3	G	rs4277404	major	-0.1453757	0.010606	0.8909245	-2.199657	1.952056	0.9600339	0.9869372
ACE	Model 3	A	rs4277404	minor	0.2876893	0.0847024	0.972951	-15.05285	18.39857	0.9600339	0.9869372
ACE	Model 3	T	rs4291	major	-0.1576506	0.0141779	0.9114151	-2.893901	2.655702	0.9869372	0.9869372
ACE	Model 3	A	rs4291	minor	-0.1108069	0.021601	0.9590764	-4.251561	4.209019	0.9869372	0.9869372
ACE	Model 3	G	rs4295	major	-0.2168719	0.0144129	0.8802951	-2.996187	2.642076	0.921877	0.9869372
ACE	Model 3	C	rs4295	minor	0.0638542	0.0213062	0.9761048	-4.028709	4.33094	0.921877	0.9869372
ACE	Model 3	G	rs4305	major	-0.2824057	0.0165645	0.8644707	-3.467825	3.008128	0.9074371	0.9869372
ACE	Model 3	A	rs4305	minor	0.0249874	0.0170649	0.9883217	-3.265182	3.427063	0.9074371	0.9869372
ACE	Model 3	G	rs4309	major	-0.3735517	0.0162189	0.8175561	-3.490712	2.84429	0.8249449	0.9869372
ACE	Model 3	A	rs4309	minor	0.221196	0.0177749	0.9010983	-3.210202	3.774244	0.8249449	0.9869372
ACE	Model 3	G	rs4311	major	-0.2391426	0.0146069	0.8698313	-3.054701	2.658187	0.9205841	0.9869372
ACE	Model 3	A	rs4311	minor	0.0467731	0.0211141	0.9823349	-4.008953	4.273858	0.9205841	0.9869372

gene	analysis	homozygote	tagsnp	alleletype	estimate	stderr	p	min95	max95	p_int	q
ACE	Model 3	G	rs4461142	major	-0.1819206	0.014425	0.8995754	-2.964499	2.68045	0.9638234	0.9869372
ACE	Model 3	A	rs4461142	minor	-0.0550687	0.020725	0.9788013	-4.033504	4.088298	0.9638234	0.9869372
PTGS1	Model 3	A	rs4836885	major	-0.1730309	0.0123372	0.8883941	-2.557951	2.270261	0.8918109	0.9869372
PTGS1	Model 3	G	rs4836885	minor	0.2259606	0.0248678	0.9276996	-4.541907	5.231971	0.8918109	0.9869372
ACE	Model 3	A	rs4968591	major	-0.1082014	0.0130987	0.9341469	-2.640084	2.489524	0.9796971	0.9869372
ACE	Model 3	G	rs4968591	minor	-0.1854414	0.0246488	0.9399885	-4.89293	4.755053	0.9796971	0.9869372
VEGFA	Model 3	G	rs735286	major	-0.0680199	0.0136183	0.9601611	-2.700059	2.635218	0.9194766	0.9869372
VEGFA	Model 3	A	rs735286	minor	-0.3694109	0.0234668	0.8747181	-4.848048	4.320028	0.9194766	0.9869372
VEGFA	Model 3	C	rs833060	major	0.0409367	0.0136124	0.9760197	-2.592854	2.745943	0.8681555	0.9869372
VEGFA	Model 3	A	rs833060	minor	-0.4540271	0.0234718	0.8463125	-4.929781	4.232438	0.8681555	0.9869372
PTGS1	Model 3	G	rs883484	major	-0.2400457	0.013118	0.8546708	-2.772262	2.35812	0.8886344	0.9869372
PTGS1	Model 3	A	rs883484	minor	0.178748	0.0242003	0.9411875	-4.461972	5.044889	0.8886344	0.9869372
ALOX15	Model 3	G	rs9894225	major	0.0278392	0.0124915	0.9822263	-2.391394	2.507033	0.8528904	0.9869372
ALOX15	Model 3	A	rs9894225	minor	-0.5161301	0.0247059	0.8341389	-5.218624	4.419673	0.8528904	0.9869372
PTGS1	Model 2	G	rs883484	major	-0.2358882	0.013143	0.8574321	-2.772971	2.367399	0.864407	0.994068
PTGS1	Model 2	A	rs883484	minor	0.2759062	0.0242453	0.9095451	-4.377744	5.156036	0.864407	0.994068
PTGS1	Model 2	G	rs10306202	major	-0.0708569	0.0118271	0.9522219	-2.360642	2.272627	0.9420858	0.9963197
PTGS1	Model 2	A	rs10306202	minor	-0.3224443	0.0308219	0.916568	-6.165681	5.884661	0.9420858	0.9963197
ALOX15	Model 2	A	rs1076039	major	-0.1216313	0.0110738	0.9125078	-2.266061	2.069851	0.9363292	0.9963197
ALOX15	Model 2	T	rs1076039	minor	0.2848002	0.0480284	0.9527935	-8.724701	10.1836	0.9363292	0.9963197
GRK4	Model 2	G	rs1801058	major	-0.0775936	0.0147302	0.9579838	-2.911168	2.849273	0.9394242	0.9963197
GRK4	Model 2	A	rs1801058	minor	-0.2908155	0.0204828	0.8869609	-4.214415	3.793503	0.9394242	0.9963197
TLR4	Model 2	A	rs1927906	major	-0.085702	0.0117152	0.9416729	-2.353734	2.235009	0.9351172	0.9963197
TLR4	Model 2	G	rs1927906	minor	-0.3602761	0.0302197	0.9049554	-6.090519	5.719619	0.9351172	0.9963197
AGT	Model 2	G	rs2478545	major	-0.0939198	0.0137255	0.9454338	-2.745719	2.630186	0.9963197	0.9963197
AGT	Model 2	A	rs2478545	minor	-0.1068363	0.0216731	0.9606735	-4.261281	4.227885	0.9963197	0.9963197
ACE	Model 2	G	rs4277404	major	-0.1181221	0.0106285	0.9114783	-2.177296	1.984397	0.9944208	0.9963197
ACE	Model 2	A	rs4277404	minor	-0.0576746	0.0848657	0.9945774	-15.37248	18.02861	0.9944208	0.9963197
ACE	Model 2	T	rs4291	major	-0.0732373	0.0142042	0.9588744	-2.816808	2.747787	0.9590476	0.9963197
ACE	Model 2	A	rs4291	minor	-0.2203669	0.0216407	0.9188231	-4.364024	4.102824	0.9590476	0.9963197
ACE	Model 2	G	rs4295	major	-0.1504922	0.0144428	0.9169704	-2.937342	2.716373	0.9614868	0.9963197
ACE	Model 2	C	rs4295	minor	-0.0119921	0.0213519	0.9955196	-4.110035	4.261189	0.9614868	0.9963197
ACE	Model 2	G	rs4305	major	-0.1423957	0.0165898	0.9315678	-3.337096	3.157889	0.9843653	0.9963197
ACE	Model 2	A	rs4305	minor	-0.0905433	0.0170833	0.9577225	-3.380391	3.311322	0.9843653	0.9963197
ACE	Model 2	G	rs4311	major	-0.1390948	0.0146359	0.924252	-2.962985	2.766974	0.9821948	0.9963197
ACE	Model 2	A	rs4311	minor	-0.0749753	0.0211587	0.9717296	-4.134146	4.15607	0.9821948	0.9963197
ACE	Model 2	G	rs4461142	major	-0.2105066	0.0144465	0.8840547	-2.996377	2.655372	0.9281605	0.9963197
ACE	Model 2	A	rs4461142	minor	0.0419922	0.0207538	0.9838645	-3.945732	4.195268	0.9281605	0.9963197
PTGS1	Model 2	A	rs4836885	major	-0.0300307	0.0123602	0.9806183	-2.422762	2.421374	0.9568741	0.9963197
PTGS1	Model 2	G	rs4836885	minor	-0.1885397	0.0248897	0.9395763	-4.940783	4.80128	0.9568741	0.9963197
ACE	Model 2	A	rs4968591	major	-0.1003012	0.0131232	0.9390612	-2.637048	2.502539	0.9885234	0.9963197
ACE	Model 2	G	rs4968591	minor	-0.1440315	0.0246863	0.9534523	-4.860476	4.806227	0.9885234	0.9963197
VEGFA	Model 2	G	rs735286	major	-0.1049716	0.0136406	0.9386428	-2.740284	2.601746	0.9772951	0.9963197
VEGFA	Model 2	A	rs735286	minor	-0.1900447	0.0235203	0.9355564	-4.686738	4.518795	0.9772951	0.9963197
VEGFA	Model 2	C	rs833060	major	-0.0256262	0.0136346	0.9850065	-2.661895	2.682042	0.9454898	0.9963197
VEGFA	Model 2	A	rs833060	minor	-0.2299494	0.0235131	0.9220243	-4.723495	4.475526	0.9454898	0.9963197

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 4	hapGCAGGGGGGTCGAGG	one	8.678101	0.0268813	0.0020173	3.100477	14.55747	0.0019685	0.059055
AGTR1	Model 4	hapGCAGGGGGGTCGAGG	zero	-0.3184767	0.0101225	0.7527332	-2.276646	1.67893	0.0019685	0.059055
AGTR1	Model 5	hapGCAGGGGGGTCGAGG	one	8.642303	0.0272775	0.0024372	2.986494	14.60872	0.0019201	0.076804
AGTR1	Model 5	hapGCAGGGGGGTCGAGG	zero	-0.4559097	0.0100236	0.6485797	-2.392467	1.519069	0.0019201	0.076804
AGTR1	Model 2	hapGCAGGGGGGTCGAGG	one	7.976804	0.0278601	0.0059814	2.238842	14.0368	0.0041817	0.250902
AGTR1	Model 2	hapGCAGGGGGGTCGAGG	zero	-0.6456773	0.0108108	0.5491845	-2.728735	1.481989	0.0041817	0.250902
ACE	Model 4	hapACCAGAGGAAGAAAAGA	one	-2.229955	0.0214496	0.2933325	-6.255044	1.967958	0.4511034	0.3079608
ACE	Model 4	hapACCAGAGGAAGAAAAGA	zero	-0.3995101	0.014632	0.7844603	-3.215309	2.49821	0.4511034	0.3079608
ACE	Model 4	hapACCAGGAAGGGAGAAGA	one	-3.675371	0.0378569	0.3228295	-10.56377	3.743569	0.3742713	0.3079608
ACE	Model 4	hapACCAGGAAGGGAGAAGA	zero	-0.3910468	0.013186	0.7664189	-2.932369	2.21681	0.3742713	0.3079608
ACE	Model 4	hapTGCAGAAAGGGAAAAGA	one	0.6797339	0.0402511	0.8663798	-6.957737	8.944135	0.7136189	0.3079608
ACE	Model 4	hapTGCAGAAAGGGAAAAGA	zero	-0.8186935	0.0133297	0.5375631	-3.376322	1.806636	0.7136189	0.3079608
ACE	Model 4	hapTGCAGAAAGGGAGTGG	one	4.297184	0.0451406	0.3515259	-4.533967	13.94527	0.2492915	0.3079608
ACE	Model 4	hapTGCAGAAAGGGAGTGG	zero	-1.074339	0.0133137	0.4173831	-3.622359	1.541045	0.2492915	0.3079608
ACE	Model 4	hapTGCAGAAAGGGAGTGG	one	-4.481478	0.0355929	0.197982	-10.91781	2.419888	0.2471891	0.3079608
ACE	Model 4	hapTGCAGAAAGGGAGTGG	zero	-0.3243135	0.0135501	0.8105862	-2.936625	2.358304	0.2471891	0.3079608
ACE	Model 4	hapwaste	one	-0.683035	0.0135965	0.6143134	-3.294744	1.999209	0.7235916	0.3079608
ACE	Model 4	hapwaste	zero	-1.281036	0.0174056	0.4590231	-4.591979	2.144807	0.7235916	0.3079608
ADRB2	Model 4	hapAGAC	one	1.434813	0.0117828	0.2269233	-0.8808617	3.804589	0.0764205	0.3079608
ADRB2	Model 4	hapAGAC	zero	-1.0392	0.0122684	0.3947021	-3.390386	1.369206	0.0764205	0.3079608
ADRB2	Model 4	hapAGAG	one	-2.735873	0.0297392	0.3511623	-8.24312	3.101918	0.266522	0.3079608
ADRB2	Model 4	hapAGAG	zero	0.6572801	0.010199	0.5207953	-1.334847	2.68963	0.266522	0.3079608
ADRB2	Model 4	hapGCGC	one	0.9403543	0.0126082	0.4580559	-1.523485	3.465838	0.410912	0.3079608
ADRB2	Model 4	hapGCGC	zero	-0.2623022	0.0118897	0.825214	-2.559665	2.089226	0.410912	0.3079608
ADRB2	Model 4	hapGGAC	one	-1.747133	0.0162535	0.2784359	-4.827769	1.433219	0.1057496	0.3079608
ADRB2	Model 4	hapGGAC	zero	1.033825	0.0107015	0.3367373	-1.063249	3.175348	0.1057496	0.3079608
ADRB2	Model 4	hapGGGG	one	-0.0876105	0.0109621	0.9362884	-2.211372	2.082275	0.5290772	0.3079608
ADRB2	Model 4	hapGGGG	zero	0.7320713	0.0127541	0.5675194	-1.754772	3.281863	0.5290772	0.3079608
ADRB2	Model 4	hapwaste	one	1.323411	0.0307444	0.6690105	-4.601806	7.616646	0.718144	0.3079608
ADRB2	Model 4	hapwaste	zero	0.1865448	0.0100632	0.8531095	-1.770128	2.182193	0.718144	0.3079608
AGT	Model 4	hapAAGCGAAGA	one	-0.6021876	0.0114218	0.5970478	-2.802618	1.648057	0.1342377	0.3079608
AGT	Model 4	hapAAGCGAAGA	zero	1.393163	0.0123036	0.2610685	-1.022647	3.867938	0.1342377	0.3079608
AGT	Model 4	hapAGAAGGGGA	one	1.23906	0.0151065	0.4151648	-1.714499	4.281375	0.3825535	0.3079608
AGT	Model 4	hapAGAAGGGGA	zero	-0.233582	0.0111329	0.8336657	-2.386917	1.967256	0.3825535	0.3079608
AGT	Model 4	hapAGGAGGGGAG	one	1.324082	0.0137398	0.3386187	-1.368118	4.089768	0.3523285	0.3079608
AGT	Model 4	hapAGGAGGGGAG	zero	-0.1633329	0.0115265	0.8872526	-2.393512	2.117802	0.3523285	0.3079608
AGT	Model 4	hapAGGCAGGG	one	-0.8034321	0.0206578	0.6962535	-4.739532	3.295305	0.557555	0.3079608
AGT	Model 4	hapAGGCAGGG	zero	0.4513768	0.0103817	0.6645242	-1.571921	2.516266	0.557555	0.3079608
AGT	Model 4	hapGGGCAGGAG	one	-0.6906087	0.0209585	0.7409735	-4.68737	3.47375	0.6203904	0.3079608
AGT	Model 4	hapGGGCAGGAG	zero	0.4042241	0.0104921	0.7006975	-1.639412	2.490321	0.6203904	0.3079608
AGT	Model 4	hapwaste	one	1.997506	0.0177806	0.2662567	-1.495811	5.61471	0.2302307	0.3079608
AGT	Model 4	hapwaste	zero	-0.2848205	0.01062	0.7883121	-2.338922	1.812485	0.2302307	0.3079608
AGTR1	Model 4	hapAAGAAAAAAAGAAGA	one	-3.638031	0.0294734	0.208919	-9.046828	2.092415	0.1512709	0.3079608
AGTR1	Model 4	hapAAGAAAAAAAGAAGA	zero	0.5658273	0.0099965	0.5725897	-1.385366	2.555627	0.1512709	0.3079608
AGTR1	Model 4	hapAAGAAGGGGAGAAGA	one	1.225992	0.0160085	0.4467276	-1.900768	4.452412	0.4755682	0.3079608
AGTR1	Model 4	hapAAGAAGGGGAGAAGA	zero	-0.0304575	0.010897	0.9777039	-2.142938	2.127626	0.4755682	0.3079608
AGTR1	Model 4	hapAAGGAGGGGAGAAGA	one	-0.2229485	0.0128321	0.86195	-2.701085	2.318304	0.5969812	0.3079608
AGTR1	Model 4	hapAAGGAGGGGAGAAGA	zero	0.5407466	0.0115799	0.641522	-1.715436	2.848722	0.5969812	0.3079608

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
AGTR1	Model 4	hapAAGGAGGGGAGAAGG	one	-1.28646	0.0254189	0.6105929	-6.083879	3.75602	0.4859756	0.3079608
AGTR1	Model 4	hapAAGGAGGGGAGAAGG	zero	0.5061989	0.010028	0.6147169	-1.449925	2.50115	0.4859756	0.3079608
ALOX15	Model 4	hapAAAGAACAAAGA	one	2.996998	0.0211693	0.1633489	-1.189025	7.360358	0.1481101	0.3079608
ALOX15	Model 4	hapAAAGAACAAAGA	zero	-0.3284833	0.0105569	0.7553589	-2.369615	1.755322	0.1481101	0.3079608
ALOX15	Model 4	hapAAAGAACAGA	one	-0.6009191	0.0262515	0.8184505	-5.585859	4.647219	0.7390392	0.3079608
ALOX15	Model 4	hapAAAGAACAGA	zero	0.317238	0.0103323	0.7592494	-1.693839	2.369456	0.7390392	0.3079608
ALOX15	Model 4	hapAAAGAGGCAG	one	-1.723912	0.0297885	0.559511	-7.297412	4.18468	0.47734	0.3079608
ALOX15	Model 4	hapAAAGAGGCAG	zero	0.3877754	0.0099533	0.6974775	-1.551629	2.365385	0.47734	0.3079608
ALOX15	Model 4	hapAAAGGACAAGA	one	2.357927	0.0365632	0.524007	-4.720637	9.962378	0.5462411	0.3079608
ALOX15	Model 4	hapAAAGGACAAGA	zero	0.0918794	0.009987	0.9267508	-1.848286	2.070396	0.5462411	0.3079608
ALOX15	Model 4	hapAAGAACGCAGA	one	-0.8806724	0.0125957	0.4826663	-3.297681	1.596747	0.1579644	0.3079608
ALOX15	Model 4	hapAAGAACGCAGA	zero	1.219835	0.0119731	0.3114716	-1.127813	3.623227	0.1579644	0.3079608
ALOX15	Model 4	hapAGAGAGGCAG	one	-1.722204	0.0290001	0.5492862	-7.152449	4.025632	0.4731044	0.3079608
ALOX15	Model 4	hapAGAGAGGCAG	zero	0.3704045	0.0100213	0.7122559	-1.581782	2.361313	0.4731044	0.3079608
ALOX15	Model 4	hapTAAAAGGCAG	one	5.953948	0.034304	0.0921209	-0.9356236	13.32266	0.0879318	0.3079608
ALOX15	Model 4	hapTAAAAGGCAG	zero	-0.2186755	0.010089	0.8282651	-2.172376	1.774042	0.0879318	0.3079608
EDN1	Model 4	hapAAGA	one	1.411427	0.023401	0.5493556	-3.134777	6.170999	0.5948356	0.3079608
EDN1	Model 4	hapAAGA	zero	0.0804982	0.0104784	0.9388046	-1.953927	2.157138	0.5948356	0.3079608
EDN1	Model 4	hapAGAC	one	-0.2289189	0.0100008	0.8187886	-2.165503	1.745999	0.1115003	0.3079608
EDN1	Model 4	hapAGAC	zero	1.756007	0.0142932	0.2235499	-1.05504	4.646917	0.1115003	0.3079608
EDN1	Model 4	hapAGGC	one	0.4762075	0.0109316	0.6639549	-1.653661	2.652202	0.5075272	0.3079608
EDN1	Model 4	hapAGGC	zero	-0.3671121	0.012592	0.7702856	-2.79594	2.122405	0.5075272	0.3079608
EDN1	Model 4	hapCAGA	one	1.187435	0.0162468	0.4676615	-1.983932	4.461413	0.4575832	0.3079608
EDN1	Model 4	hapCAGA	zero	-0.1826163	0.011219	0.8706123	-2.353533	2.036565	0.4575832	0.3079608
EDN1	Model 4	hapCGGC	one	1.703179	0.0359865	0.6389598	-5.223048	9.135569	0.6805283	0.3079608
EDN1	Model 4	hapCGGC	zero	0.1770832	0.0100703	0.8605723	-1.780774	2.173968	0.6805283	0.3079608
EDN1	Model 4	hapwaste	one	-2.942677	0.0368875	0.4182958	-9.712084	4.334271	0.3670636	0.3079608
EDN1	Model 4	hapwaste	zero	0.4271693	0.0101083	0.6733409	-1.542908	2.436667	0.3670636	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACGA	one	0.6307182	0.0115923	0.5876808	-1.62988	2.943266	0.5285385	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACGA	zero	-0.2200554	0.012215	0.8569137	-2.580506	2.197589	0.5285385	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACAGAAG	one	0.9704468	0.0153451	0.5292528	-2.021107	4.05334	0.5722448	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACAGAAG	zero	0.0234661	0.0108635	0.9827727	-2.083726	2.176006	0.5722448	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACAGCAG	one	-0.2511204	0.0189136	0.894268	-3.881109	3.515957	0.7364632	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACGGACGA	zero	0.4246741	0.0105719	0.6886175	-1.634779	2.527245	0.7364632	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACGGGAAG	one	2.339571	0.0236347	0.3280708	-2.292992	7.191777	0.3385997	0.3079608
GRK4	Model 4	hapACAGGAGCAAGAACGGGAAG	zero	-0.0288028	0.0102528	0.9775906	-2.017681	2.000446	0.3385997	0.3079608
GRK4	Model 4	hapACGGGAACAAAACAGACGA	one	-2.4036	0.0263628	0.356296	-7.31836	2.771782	0.2783683	0.3079608
GRK4	Model 4	hapACGGGAACAAAACAGACGA	zero	0.5386379	0.0102446	0.6001411	-1.459955	2.577766	0.2783683	0.3079608
GRK4	Model 4	hapTGGAGTAAGGAACAAGAAG	one	-1.575144	0.0236947	0.5029752	-6.041546	3.103572	0.3930525	0.3079608
GRK4	Model 4	hapTGGAGTAAGGAACAAGAAG	zero	0.524388	0.0103133	0.6121747	-1.487175	2.577025	0.3930525	0.3079608
GRK4	Model 4	hapTGGAGTAAGGAACAGGAAG	one	-1.523367	0.0167965	0.3609721	-4.712487	1.772488	0.2157455	0.3079608
GRK4	Model 4	hapTGGAGTAAGGAACAGGAAG	zero	0.7006536	0.0107276	0.5152912	-1.394549	2.840375	0.2157455	0.3079608
GRK4	Model 4	hapwaste	one	0.5297472	0.0126367	0.6759602	-1.929549	3.050715	0.7353969	0.3079608
GRK4	Model 4	hapwaste	zero	0.0553628	0.0115216	0.9616957	-2.178767	2.340518	0.7353969	0.3079608
PTGS1	Model 4	hapGAGAGGGGCAG	one	0.5400925	0.0122712	0.6607957	-1.849161	2.987506	0.6760219	0.3079608
PTGS1	Model 4	hapGAGAGGGGCAG	zero	-0.0408848	0.0117768	0.9723072	-2.321732	2.293222	0.6760219	0.3079608
PTGS1	Model 4	hapGGGAGGGCAGG	one	-2.046527	0.0236801	0.382762	-6.488875	2.60686	0.2709354	0.3079608
PTGS1	Model 4	hapGGGAGGGCAGG	zero	0.5883231	0.0101185	0.5622287	-1.386887	2.603096	0.2709354	0.3079608

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
PTGS1	Model 4	hapGGGAGGGGCAG	one	0.9344062	0.0115995	0.4228486	-1.334404	3.255387	0.342282	0.3079608
PTGS1	Model 4	hapGGGAGGGGCAG	zero	-0.3937796	0.0124852	0.7520538	-2.801618	2.073707	0.342282	0.3079608
PTGS1	Model 4	hapGGGGGAGCAGA	one	-5.15078	0.0517371	0.3069702	-14.29719	4.971759	0.2679816	0.3079608
PTGS1	Model 4	hapGGGGGAGCAGA	zero	0.4839663	0.0098149	0.6228939	-1.430547	2.435665	0.2679816	0.3079608
PTGS1	Model 4	hapGGGGGAGGCAG	one	-1.076402	0.0297276	0.7158966	-6.675486	4.858603	0.6525189	0.3079608
PTGS1	Model 4	hapGGGGGAGGCAG	zero	0.2776931	0.0100286	0.7822073	-1.674084	2.268214	0.6525189	0.3079608
PTGS1	Model 4	hapGGGGGGGGCAG	one	-1.268477	0.0179534	0.4772148	-4.682231	2.26754	0.3237954	0.3079608
PTGS1	Model 4	hapGGGGGGGGCAG	zero	0.6708995	0.010879	0.5389388	-1.452935	2.840505	0.3237954	0.3079608
PTGS1	Model 4	hapwaste	one	0.3430142	0.0111664	0.759168	-1.829217	2.56331	0.7047932	0.3079608
PTGS1	Model 4	hapwaste	zero	-0.1188766	0.0119673	0.9208454	-2.434366	2.251565	0.7047932	0.3079608
PTGS2	Model 4	hapAGC	one	2.764047	0.0208275	0.1908001	-1.346429	7.045788	0.1616794	0.3079608
PTGS2	Model 4	hapAGC	zero	-0.3334958	0.0104314	0.7488543	-2.3505	1.725171	0.1616794	0.3079608
PTGS2	Model 4	hapCAA	one	-2.353416	0.0374491	0.5249587	-9.26385	5.083313	0.4695101	0.3079608
PTGS2	Model 4	hapCAA	zero	0.416207	0.0101588	0.6827378	-1.563401	2.435626	0.4695101	0.3079608
PTGS2	Model 4	hapCGA	one	0.7634119	0.0150341	0.6130681	-2.162397	3.776717	0.6534665	0.3079608
PTGS2	Model 4	hapCGA	zero	1.513521	0.0295772	0.6116458	-4.203913	7.57219	0.6534665	0.3079608
PTGS2	Model 4	hapwaste	one	-0.9462948	0.0283686	0.7375752	-6.303508	4.717224	0.6479387	0.3079608
PTGS2	Model 4	hapwaste	zero	0.3862361	0.0101927	0.705359	-1.59931	2.411847	0.6479387	0.3079608
TLR4	Model 4	hapAAGGCCAA	one	-1.250013	0.0162607	0.4393638	-4.347589	1.947875	0.2732982	0.3079608
TLR4	Model 4	hapAAGGCCAA	zero	0.7696109	0.011267	0.4963756	-1.431279	3.019643	0.2732982	0.3079608
TLR4	Model 4	hapAAGGCCAA	one	0.6451258	0.0113768	0.572044	-1.574243	2.914538	0.5539848	0.3079608
TLR4	Model 4	hapAAGGCCAA	zero	-0.1868405	0.0127997	0.8838646	-2.659696	2.348836	0.5539848	0.3079608
TLR4	Model 4	hapAGAACGCAA	one	2.227843	0.0172355	0.2014059	-1.167831	5.740185	0.1916976	0.3079608
TLR4	Model 4	hapAGAACGCAA	zero	-0.2329065	0.0107352	0.8280905	-2.310143	1.8885	0.1916976	0.3079608
TLR4	Model 4	hapAGAAAGCGG	one	-1.807478	0.0231991	0.4319125	-6.172255	2.760343	0.3209756	0.3079608
TLR4	Model 4	hapAGAAAGCGG	zero	0.5623702	0.010264	0.5849321	-1.440429	2.605868	0.3209756	0.3079608
TLR4	Model 4	hapAGAGAGCAA	one	3.598709	0.0331397	0.2863035	-2.916424	10.55106	0.2975967	0.3079608
TLR4	Model 4	hapAGAGAGCAA	zero	0.0035561	0.0101013	0.9971918	-1.956855	2.003167	0.2975967	0.3079608
TLR4	Model 4	hapAGAGAGCGG	one	2.598695	0.0249523	0.3041231	-2.298242	7.741071	0.3081878	0.3079608
TLR4	Model 4	hapAGAGAGCGG	zero	0.0443659	0.0100065	0.9646524	-1.898625	2.02584	0.3081878	0.3079608
TLR4	Model 4	hapwaste	one	-0.7533689	0.0167189	0.6511402	-3.952817	2.552657	0.4351921	0.3079608
TLR4	Model 4	hapwaste	zero	0.6142206	0.0106054	0.5638068	-1.455572	2.727486	0.4351921	0.3079608
VEGFA	Model 4	hapAAACAAAGGAG	one	2.757528	0.0233102	0.2435078	-1.831542	7.561122	0.2441761	0.3079608
VEGFA	Model 4	hapAAACAAAGGAG	zero	-0.0754112	0.0102214	0.9411798	-2.057336	1.946619	0.2441761	0.3079608
VEGFA	Model 4	hapCTAACGAAAG	one	1.174491	0.0305902	0.7027602	-4.713225	7.426005	0.7391059	0.3079608
VEGFA	Model 4	hapCTAACGAAAG	zero	0.1422858	0.0099281	0.8861495	-1.787513	2.110004	0.7391059	0.3079608
VEGFA	Model 4	hapCTACAAAGGAG	one	-0.4682044	0.0187561	0.8024731	-4.06068	3.258793	0.6663925	0.3079608
VEGFA	Model 4	hapCTACAAAGGAG	zero	0.3876944	0.0105442	0.7137162	-1.665652	2.483917	0.6663925	0.3079608
VEGFA	Model 4	hapCTACAAAGGG	one	-3.837345	0.0293401	0.182626	-9.211229	1.854625	0.1275371	0.3079608
VEGFA	Model 4	hapCTACAAAGGG	zero	0.6324258	0.0100204	0.5293934	-1.324671	2.628339	0.1275371	0.3079608
VEGFA	Model 4	hapCTACCGAGAAA	one	-1.158027	0.026653	0.6621922	-6.18887	4.142607	0.576538	0.3079608
VEGFA	Model 4	hapCTACCGAGAAA	zero	0.3669296	0.0101463	0.7181929	-1.609289	2.382841	0.576538	0.3079608
VEGFA	Model 4	hapCTACCGAGAG	one	2.490753	0.0155345	0.113574	-0.5827695	5.659294	0.0725229	0.3079608
VEGFA	Model 4	hapCTACCGAGAG	zero	-0.6774781	0.0111556	0.5424196	-2.825545	1.518072	0.0725229	0.3079608
VEGFA	Model 4	hapCTACGGGGAAA	one	1.533713	0.0355375	0.6685253	-5.297663	8.857873	0.6821236	0.3079608
VEGFA	Model 4	hapCTACGGGGAAA	zero	0.0643108	0.0098727	0.9480921	-1.853327	2.019417	0.6821236	0.3079608
VEGFA	Model 4	hapCTGACGGAAAA	one	-4.298135	0.0265832	0.0987195	-9.156738	0.8203229	0.0739003	0.3079608
VEGFA	Model 4	hapCTGACGGAAAA	zero	0.5513173	0.0101711	0.5889358	-1.433325	2.57592	0.0739003	0.3079608

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
VEGFA	Model 4	hapCTGACGGAAAG	one	-0.3149379	0.0174509	0.8565964	-3.666836	3.153589	0.7180547	0.3079608
VEGFA	Model 4	hapCTGACGGAAAG	zero	0.3722895	0.010835	0.7316989	-1.736755	2.526601	0.7180547	0.3079608
VEGFA	Model 4	hapwaste	one	-0.0204948	0.0108394	0.984917	-2.122149	2.126286	0.5552816	0.3079608
VEGFA	Model 4	hapwaste	zero	0.699348	0.0124174	0.5747603	-1.721856	3.180201	0.5552816	0.3079608
ACE	Model 4	hapTGCAGAGAAAAGGAAGA	one	-2.197384	0.050232	0.6583502	-11.36752	7.921513	0.7585154	0.3086028
ACE	Model 4	hapTGCAGAGAAAAGGAAGA	zero	-0.6326352	0.0134708	0.6376529	-3.221825	2.025826	0.7585154	0.3086028
ACE	Model 4	hapTGCAGAGAAAAGGAAGA	one	-0.5451169	0.0144435	0.7051805	-3.321087	2.31056	0.7817938	0.3086028
ACE	Model 4	hapTGCAGAGAAAAGGAAGA	zero	-1.0393	0.0168395	0.5351301	-4.252166	2.281376	0.7817938	0.3086028
ALOX15	Model 4	hapAAAGAACGAGG	one	-0.0438659	0.0142289	0.9754068	-2.792935	2.782948	0.7623547	0.3086028
ALOX15	Model 4	hapAAAGAACGAGG	zero	0.4361231	0.0112606	0.6992401	-1.756259	2.677429	0.7623547	0.3086028
ALOX15	Model 4	hapwaste	one	0.4086685	0.0117198	0.727923	-1.871477	2.741796	0.7777244	0.3086028
ALOX15	Model 4	hapwaste	zero	0.0360001	0.0118991	0.9758744	-2.270017	2.39643	0.7777244	0.3086028
AGT	Model 4	hapGGGCAGGG	one	-0.0014653	0.0185105	0.9993685	-3.564389	3.693094	0.8735905	0.3247728
AGT	Model 4	hapGGGCAGGG	zero	0.3291816	0.0110509	0.7662314	-1.820516	2.525948	0.8735905	0.3247728
AGTR1	Model 4	hapAAGAAAGAACATCGGG	one	-0.2146602	0.0384048	0.9553895	-7.449981	7.586299	0.898538	0.3247728
AGTR1	Model 4	hapAAGAAAGAACATCGGG	zero	0.2841528	0.0100119	0.7769201	-1.664543	2.271466	0.898538	0.3247728
AGTR1	Model 4	hapwaste	one	0.2554131	0.0098122	0.7949398	-1.654223	2.20213	0.8716936	0.3247728
AGTR1	Model 4	hapwaste	zero	0.067238	0.0155045	0.9654295	-2.927896	3.154786	0.8716936	0.3247728
ALOX15	Model 4	hapAAAAAGGCGAG	one	0.9991421	0.0306579	0.7457918	-4.890998	7.254061	0.8415458	0.3247728
ALOX15	Model 4	hapAAAAAGGCGAG	zero	0.3696433	0.0100902	0.7146932	-1.595808	2.374351	0.8415458	0.3247728
ALOX15	Model 4	hapAAAGAACGCGAG	one	0.5776564	0.0264455	0.8276264	-4.502716	5.9283	0.8939164	0.3247728
ALOX15	Model 4	hapAAAGAACGCGAG	zero	0.2148236	0.0101422	0.8324746	-1.757614	2.226862	0.8939164	0.3247728
TLR4	Model 4	hapGAGGCCGCAA	one	0.0411268	0.0173365	0.9810824	-3.301062	3.498831	0.8705845	0.3247728
TLR4	Model 4	hapGAGGCCGCAA	zero	0.340041	0.0105855	0.7485133	-1.720279	2.443554	0.8705845	0.3247728
VEGFA	Model 4	hapCTGACGGAAGG	one	-0.0743948	0.0228297	0.9740009	-4.447055	4.498366	0.877591	0.3247728
VEGFA	Model 4	hapCTGACGGAAGG	zero	0.2858392	0.0101776	0.7791892	-1.694807	2.306392	0.877591	0.3247728
ACE	Model 4	hapACCAGAGGAAAGATGGG	one	-0.4452329	0.028061	0.8736852	-5.772761	5.183509	0.9192707	0.328311
ACE	Model 4	hapACCAGAGGAAAGATGGG	zero	-0.7388481	0.0136983	0.5883713	-3.368379	1.962237	0.9192707	0.328311
TLR4	Model 4	hapAGAGAGGGAG	one	0.1397456	0.0195428	0.943048	-3.623402	4.04983	0.9491082	0.3349794
TLR4	Model 4	hapAGAGAGGGAG	zero	0.2742113	0.0106585	0.7972945	-1.79881	2.390994	0.9491082	0.3349794
VEGFA	Model 4	hapCTAACAAAGAAG	one	0.2975521	0.0259352	0.908818	-4.67337	5.527689	0.9957928	0.3473696
VEGFA	Model 4	hapCTAACAAAGAAG	zero	0.2835064	0.0101515	0.7803941	-1.692068	2.298782	0.9957928	0.3473696
ACE	Model 5	hapACCGAGGAAAGGGAGAAGA	one	-4.712573	0.0360318	0.180644	-11.20976	2.260038	0.2270975	0.4068428
ACE	Model 5	hapACCGAGGAAAGGGAGAAGA	zero	-0.4776284	0.0130953	0.7147357	-2.999494	2.109802	0.2270975	0.4068428
ACE	Model 5	hapTGCAGAGAAGGGAGTGGG	one	4.031769	0.044499	0.3746222	-4.657101	13.51248	0.2536555	0.4068428
ACE	Model 5	hapTGCAGAGAAGGGAGTGGG	zero	-1.190144	0.0131622	0.3632317	-3.706578	1.392051	0.2536555	0.4068428
ACE	Model 5	hapTGCAGAGAAGGGAGTGGG	one	-4.169503	0.0351745	0.226259	-10.55353	2.670172	0.3016228	0.4068428
ACE	Model 5	hapTGCAGAGAAGGGAGTGGG	zero	-0.4957559	0.0134331	0.7114816	-3.081362	2.158829	0.3016228	0.4068428
ADRB2	Model 5	hapAGAC	one	1.448355	0.0117434	0.2210552	-0.8599706	3.810426	0.0464381	0.4068428
ADRB2	Model 5	hapAGAC	zero	-1.31153	0.0121428	0.2771947	-3.632525	1.065367	0.0464381	0.4068428
ADRB2	Model 5	hapAGAG	one	-2.921532	0.0296066	0.316835	-8.394463	2.878377	0.2552791	0.4068428
ADRB2	Model 5	hapAGAG	zero	0.5386142	0.0101445	0.5965637	-1.440634	2.55761	0.2552791	0.4068428
ADRB2	Model 5	hapGCGC	one	0.882929	0.0124967	0.4819542	-1.557998	3.384381	0.3626654	0.4068428
ADRB2	Model 5	hapGCGC	zero	-0.442201	0.011857	0.7086527	-2.729172	1.89854	0.3626654	0.4068428
ADRB2	Model 5	hapGGAC	one	-1.954624	0.0162629	0.2251133	-5.030503	1.220878	0.0932538	0.4068428
ADRB2	Model 5	hapGGAC	zero	0.9350471	0.0106395	0.3819144	-1.147962	3.06195	0.0932538	0.4068428
ADRB2	Model 5	hapGGGG	one	-0.3371384	0.010882	0.7563705	-2.440277	1.811338	0.37974	0.4068428
ADRB2	Model 5	hapGGGG	zero	0.8039228	0.0127136	0.5289658	-1.676887	3.347327	0.37974	0.4068428

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
AGT	Model 5	hapAAGCGAAGA	one	-0.4408049	0.0113208	0.6964459	-2.625542	1.79295	0.3185006	0.4068428
AGT	Model 5	hapAAGCGAAGA	zero	0.8745604	0.0122492	0.4773329	-1.518404	3.32567	0.3185006	0.4068428
AGT	Model 5	hapAGGAGGGAG	one	1.204163	0.0136955	0.3823334	-1.476283	3.957533	0.3454734	0.4068428
AGT	Model 5	hapAGGAGGGAG	zero	-0.2925042	0.0114245	0.797689	-2.500304	1.96529	0.3454734	0.4068428
AGT	Model 5	hapwaste	one	1.400993	0.0177469	0.4332558	-2.065436	4.990116	0.3823831	0.4068428
AGT	Model 5	hapwaste	zero	-0.2546143	0.0105543	0.8091789	-2.296761	1.830217	0.3823831	0.4068428
AGTR1	Model 5	hapAAGAAAAAAAGAAGA	one	-3.399772	0.030083	0.2505069	-8.930818	2.467199	0.2032516	0.4068428
AGTR1	Model 5	hapAAGAAAAAAAGAAGA	zero	0.409083	0.00991	0.6804615	-1.522377	2.378426	0.2032516	0.4068428
ALOX15	Model 5	hapAAAGAACAAAGA	one	3.112445	0.020997	0.1446794	-1.044845	7.44439	0.1120303	0.4068428
ALOX15	Model 5	hapAAAGAACAAAGA	zero	-0.4942886	0.0104357	0.6350157	-2.508871	1.561923	0.1120303	0.4068428
ALOX15	Model 5	hapAAGAACGCAGA	one	-0.9710392	0.0125691	0.437733	-3.380803	1.498827	0.1711161	0.4068428
ALOX15	Model 5	hapAAGAACGCAGA	zero	1.046373	0.0118256	0.3789417	-1.268723	3.415755	0.1711161	0.4068428
ALOX15	Model 5	hapAGAGAGGCAG	one	-2.290884	0.0292644	0.4285904	-7.737506	3.477275	0.3820497	0.4068428
ALOX15	Model 5	hapAGAGAGGCAG	zero	0.2710267	0.0099401	0.7854536	-1.663563	2.243675	0.3820497	0.4068428
ALOX15	Model 5	hapTAAAAGGCGAG	one	5.720959	0.0335786	0.0978744	-1.012819	12.91282	0.0873372	0.4068428
ALOX15	Model 5	hapTAAAAGGCGAG	zero	-0.3288742	0.0100313	0.7426862	-2.269362	1.650143	0.0873372	0.4068428
EDN1	Model 5	hapAGAC	one	-0.3130813	0.0099832	0.7535095	-2.244658	1.656662	0.1486801	0.4068428
EDN1	Model 5	hapAGAC	zero	1.47671	0.0141187	0.2993931	-1.292874	4.324005	0.1486801	0.4068428
EDN1	Model 5	hapwaste	one	-4.055758	0.0391012	0.2899167	-11.13394	3.586206	0.261696	0.4068428
EDN1	Model 5	hapwaste	zero	0.3400277	0.0100093	0.7345788	-1.609245	2.327919	0.261696	0.4068428
GRK4	Model 5	hapACAGGAGCAAGAACAGAGAAG	one	1.231167	0.0151324	0.4189226	-1.727165	4.278555	0.3836889	0.4068428
GRK4	Model 5	hapACAGGAGCAAGAACAGAGAAG	zero	-0.2010541	0.0107581	0.8516408	-2.28334	1.925604	0.3836889	0.4068428
GRK4	Model 5	hapACAGGAGCAAGAACAGGGAAAG	one	2.410067	0.0235337	0.3118093	-2.206334	7.244388	0.2923672	0.4068428
GRK4	Model 5	hapACAGGAGCAAGAACAGGGAAAG	zero	-0.1808138	0.0101661	0.858743	-2.150046	1.828049	0.2923672	0.4068428
GRK4	Model 5	hapACGGGAACAAAACAGACGA	one	-3.042381	0.0263514	0.2412889	-7.922913	2.096844	0.1945742	0.4068428
GRK4	Model 5	hapACGGGAACAAAACAGACGA	zero	0.4684407	0.010177	0.6461761	-1.515698	2.492553	0.1945742	0.4068428
GRK4	Model 5	hapTGGAGTAAGGAACAGGAAG	one	-1.68631	0.0166578	0.3075227	-4.844295	1.576479	0.1990864	0.4068428
GRK4	Model 5	hapTGGAGTAAGGAACAGGAAG	zero	0.5908483	0.0106306	0.5795894	-1.48333	2.708697	0.1990864	0.4068428
PTGS1	Model 5	hapGGGAGGGCAGG	one	-1.821739	0.0234352	0.4329207	-6.229271	2.792961	0.3464102	0.4068428
PTGS1	Model 5	hapGGGAGGGCAGG	zero	0.4076884	0.0100439	0.6855039	-1.549573	2.403862	0.3464102	0.4068428
PTGS1	Model 5	hapGGGAGGGGCAG	one	0.7421892	0.0114401	0.5181913	-1.491534	3.026563	0.3847594	0.4068428
PTGS1	Model 5	hapGGGAGGGGCAG	zero	-0.4488709	0.0123739	0.7162531	-2.834175	1.994989	0.3847594	0.4068428
PTGS1	Model 5	hapGGGGGGAGCAGA	one	-4.966823	0.0506693	0.3149362	-13.95107	4.955452	0.2869479	0.4068428
PTGS1	Model 5	hapGGGGGGAGCAGA	zero	0.3451505	0.0097677	0.7243487	-1.557611	2.284689	0.2869479	0.4068428
PTGS1	Model 5	hapGGGGGGGGCAG	one	-1.345573	0.0176567	0.4431151	-4.701255	2.128271	0.3298942	0.4068428
PTGS1	Model 5	hapGGGGGGGGCAG	zero	0.5258743	0.010761	0.6260783	-1.572131	2.668598	0.3298942	0.4068428
PTGS2	Model 5	hapAGC	one	2.720769	0.0205881	0.1925797	-1.341697	6.950515	0.1460484	0.4068428
PTGS2	Model 5	hapAGC	zero	-0.4709543	0.0104086	0.6502616	-2.480822	1.580336	0.1460484	0.4068428
PTGS2	Model 5	hapCAA	one	-3.671884	0.0378603	0.3233405	-10.56112	3.748013	0.2951981	0.4068428
PTGS2	Model 5	hapCAA	zero	0.3622976	0.0101177	0.7208418	-1.608321	2.372384	0.2951981	0.4068428
TLR4	Model 5	hapAGAAAGGCAA	one	2.139943	0.0175867	0.2288905	-1.320753	5.722006	0.1904671	0.4068428
TLR4	Model 5	hapAGAAAGGCAA	zero	-0.3533202	0.0106076	0.7386978	-2.403642	1.740075	0.1904671	0.4068428
TLR4	Model 5	hapAGAAAGGCAG	one	-1.740317	0.022751	0.4404884	-6.025568	2.740342	0.3618756	0.4068428
TLR4	Model 5	hapAGAAAGGCAG	zero	0.4059824	0.0102468	0.6926318	-1.590399	2.442863	0.3618756	0.4068428
TLR4	Model 5	hapAGAGAGGCAA	one	3.230865	0.0332051	0.3384888	-3.27353	10.17265	0.3321684	0.4068428
TLR4	Model 5	hapAGAGAGGCAA	zero	-0.1075961	0.0100111	0.9143865	-2.04852	1.871787	0.3321684	0.4068428
TLR4	Model 5	hapAGAGAGGCAG	one	2.086217	0.0244667	0.3989262	-2.693691	7.100924	0.3865007	0.4068428
TLR4	Model 5	hapAGAGAGGCAG	zero	-0.0361277	0.0099475	0.9710306	-1.966226	1.93197	0.3865007	0.4068428

gene	analysis	haplotype	num_haplos	estimate	stder	p	min95	max95	p_int	q
TLR4	Model 5	hapwaste	one	-1.008386	0.0166399	0.54261	-4.184783	2.273313	0.3687296	0.4068428
TLR4	Model 5	hapwaste	zero	0.5628142	0.0105616	0.5952662	-1.497483	2.666205	0.3687296	0.4068428
VEGFA	Model 5	hapAAACAAAGGAG	one	2.398387	0.0232764	0.3088148	-2.168165	7.178095	0.2885168	0.4068428
VEGFA	Model 5	hapAAACAAAGGAG	zero	-0.1720544	0.0101394	0.8651736	-2.136329	1.831647	0.2885168	0.4068428
VEGFA	Model 5	hapCTACAAAGGGG	one	-3.566338	0.0292739	0.2150752	-8.943563	2.128432	0.1672124	0.4068428
VEGFA	Model 5	hapCTACAAAGGGG	zero	0.4753836	0.009942	0.6334494	-1.463523	2.452442	0.1672124	0.4068428
VEGFA	Model 5	hapCTACCGAGAAG	one	2.321162	0.0155579	0.1405558	-0.7518228	5.489295	0.0788907	0.4068428
VEGFA	Model 5	hapCTACCGAGAAG	zero	-0.789747	0.011104	0.4753637	-2.925581	1.39308	0.0788907	0.4068428
VEGFA	Model 5	hapCTGACGGAAAA	one	-4.785724	0.0271158	0.0708219	-9.713869	0.4114169	0.0571261	0.4068428
VEGFA	Model 5	hapCTGACGGAAAA	zero	0.4513937	0.0100847	0.6552637	-1.514596	2.456629	0.0571261	0.4068428
AGT	Model 5	hapAGGCAGGGA	one	-1.353819	0.0202273	0.5005475	-5.188122	2.635548	0.3998369	0.409113
AGT	Model 5	hapAGGCAGGGA	zero	0.3929995	0.0102812	0.7029128	-1.609754	2.43652	0.3998369	0.409113
ALOX15	Model 5	hapAAAGAGGCGAG	one	-2.126633	0.0293219	0.4636728	-7.592823	3.6629	0.409113	0.409113
ALOX15	Model 5	hapAAAGAGGCGAG	zero	0.2876898	0.0099073	0.7719027	-1.6409	2.254094	0.409113	0.409113
ACE	Model 5	hapACCAGAGGAAAGAAAGA	one	-1.968981	0.0206311	0.3353325	-5.853914	2.076263	0.5613968	0.4158495
ACE	Model 5	hapACCAGAGGAAAGAAAGA	zero	-0.608022	0.0145302	0.6747732	-3.398656	2.263229	0.5613968	0.4158495
AGT	Model 5	hapAGAAGGGGA	one	0.7733893	0.0153257	0.6152903	-2.208613	3.846324	0.5604767	0.4158495
AGT	Model 5	hapAGAAGGGGA	zero	-0.2166301	0.0109947	0.8436759	-2.34388	1.956958	0.5604767	0.4158495
AGTR1	Model 5	hapAAGAAGGGGAGAAGA	one	1.093301	0.0156839	0.4882827	-1.967025	4.249161	0.4709628	0.4158495
AGTR1	Model 5	hapAAGAAGGGGAGAAGA	zero	-0.1540875	0.0108441	0.8869484	-2.253824	1.990754	0.4709628	0.4158495
AGTR1	Model 5	hapAAGGAGGGGAGAAGG	one	-1.465515	0.0246168	0.5488174	-6.106738	3.405128	0.4572998	0.4158495
AGTR1	Model 5	hapAAGGAGGGGAGAAGG	zero	0.3911543	0.010004	0.6964451	-1.558085	2.37899	0.4572998	0.4158495
ALOX15	Model 5	hapAAAGGACAAGA	one	2.437316	0.035211	0.4941956	-4.393692	9.756395	0.4926038	0.4158495
ALOX15	Model 5	hapAAAGGACAAGA	zero	-0.0524953	0.0099479	0.9579144	-1.982345	1.91535	0.4926038	0.4158495
EDN1	Model 5	hapAGGC	one	0.34926	0.0108121	0.7471694	-1.754907	2.498493	0.5304728	0.4158495
EDN1	Model 5	hapAGGC	zero	-0.4410028	0.0125775	0.7253591	-2.865268	2.043766	0.5304728	0.4158495
EDN1	Model 5	hapCAGA	one	0.9354579	0.0159562	0.5596603	-2.172299	4.141941	0.5084392	0.4158495
EDN1	Model 5	hapCAGA	zero	-0.2581219	0.0111538	0.8168037	-2.414929	1.946354	0.5084392	0.4158495
EDN1	Model 5	hapCGGC	one	2.531009	0.035603	0.4828115	-4.379741	9.941218	0.4899045	0.4158495
EDN1	Model 5	hapCGGC	zero	-0.0059328	0.0099966	0.9952658	-1.946051	1.972573	0.4899045	0.4158495
GRK4	Model 5	hapACAGGAGCAAGAACAGA	one	0.5041882	0.0115955	0.6645484	-1.754182	2.814471	0.5317833	0.4158495
GRK4	Model 5	hapACAGGAGCAAGAACAGA	zero	-0.3384876	0.0120941	0.779265	-2.673087	2.052113	0.5317833	0.4158495
GRK4	Model 5	hapTGGAGTAAGGAACAAGAAG	one	-1.545183	0.0235656	0.5088851	-5.989172	3.108877	0.4309489	0.4158495
GRK4	Model 5	hapTGGAGTAAGGAACAAGAAG	zero	0.3746458	0.010217	0.7144396	-1.615356	2.404899	0.4309489	0.4158495
TLR4	Model 5	hapAAGGCGCCAA	one	-0.9291285	0.0165453	0.572751	-4.090289	2.336223	0.4495016	0.4158495
TLR4	Model 5	hapAAGGCGCCAA	zero	0.4867108	0.0111711	0.6639243	-1.689527	2.711123	0.4495016	0.4158495
TLR4	Model 5	hapAAGGCGCCAA	one	0.5460498	0.0113915	0.632724	-1.673964	2.816187	0.5270246	0.4158495
TLR4	Model 5	hapAAGGCGCCAA	zero	-0.3412525	0.012674	0.7874355	-2.786336	2.165329	0.5270246	0.4158495
VEGFA	Model 5	hapCTACCGAGAAA	one	-1.331491	0.0262702	0.6099892	-6.283221	3.881873	0.5575274	0.4158495
VEGFA	Model 5	hapCTACCGAGAAA	zero	0.2441185	0.0100698	0.8087291	-1.714954	2.242241	0.5575274	0.4158495
VEGFA	Model 5	hapwaste	one	-0.1913586	0.0107433	0.8585323	-2.271014	1.932551	0.4942043	0.4158495
VEGFA	Model 5	hapwaste	zero	0.6404871	0.0123825	0.6062463	-1.772582	3.112835	0.4942043	0.4158495
ACE	Model 5	hapwaste	one	-0.8020493	0.0134226	0.5486788	-3.377702	1.842262	0.7067844	0.4306552
ACE	Model 5	hapwaste	zero	-1.420619	0.0173498	0.4097496	-4.716453	1.989218	0.7067844	0.4306552
ADRB2	Model 5	hapwaste	one	1.591898	0.0311508	0.6122631	-4.425176	7.987787	0.6261743	0.4306552
ADRB2	Model 5	hapwaste	zero	0.0390915	0.0099813	0.9687731	-1.89896	2.015431	0.6261743	0.4306552
AGT	Model 5	hapGGCAGGAG	one	-0.7954504	0.0206317	0.6987733	-4.727005	3.298345	0.622596	0.4306552
AGT	Model 5	hapGGCAGGAG	zero	0.2724932	0.0104143	0.7939174	-1.753487	2.340253	0.622596	0.4306552

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
ALOX15	Model 5	hapAAAGAACGAGG	one	-0.217851	0.0144734	0.8802571	-3.008643	2.653242	0.7317079	0.4306552
ALOX15	Model 5	hapAAAGAACGAGG	zero	0.3361235	0.0111546	0.7636091	-1.833677	2.553884	0.7317079	0.4306552
EDN1	Model 5	hapAAGA	one	1.053624	0.0231851	0.6513213	-3.435668	5.751625	0.6673065	0.4306552
EDN1	Model 5	hapAAGA	zero	-0.0094477	0.0104093	0.9927598	-2.028776	2.051502	0.6673065	0.4306552
GRK4	Model 5	hapACAGGAGCAAGAAGGACGA	one	-0.5794435	0.018868	0.7581495	-4.188933	3.166026	0.6392758	0.4306552
GRK4	Model 5	hapACAGGAGCAAGAAGGACGA	zero	0.3567696	0.0104819	0.7341071	-1.683936	2.439833	0.6392758	0.4306552
GRK4	Model 5	hapwaste	one	0.3859347	0.0123913	0.7559754	-2.02273	2.853813	0.7428803	0.4306552
GRK4	Model 5	hapwaste	zero	-0.0654222	0.0115091	0.9546662	-2.294456	2.214465	0.7428803	0.4306552
PTGS1	Model 5	hapGAGAGGGGCAG	one	0.4754784	0.0122907	0.6996197	-1.915979	2.925244	0.6272425	0.4306552
PTGS1	Model 5	hapGAGAGGGGCAG	zero	-0.2001015	0.0116753	0.8638177	-2.457904	2.109962	0.6272425	0.4306552
PTGS1	Model 5	hapGGGGGAGGCAG	one	-1.279379	0.0299415	0.6672526	-6.90602	4.687338	0.6379251	0.4306552
PTGS1	Model 5	hapGGGGGAGGCAG	zero	0.1484557	0.0099683	0.8817275	-1.789199	2.12434	0.6379251	0.4306552
PTGS2	Model 5	hapCGA	one	0.5773323	0.0150131	0.7014711	-2.339059	3.580814	0.6947262	0.4306552
PTGS2	Model 5	hapCGA	zero	1.235618	0.0296747	0.6790828	-4.484421	7.298206	0.6947262	0.4306552
PTGS2	Model 5	hapwaste	one	-0.9025058	0.028661	0.7518266	-6.315802	4.823584	0.696968	0.4306552
PTGS2	Model 5	hapwaste	zero	0.2438767	0.0101181	0.8098095	-1.724498	2.251676	0.696968	0.4306552
VEGFA	Model 5	hapCTAACGAAAG	one	1.342697	0.0307165	0.6642248	-4.578439	7.631255	0.6644103	0.4306552
VEGFA	Model 5	hapCTAACGAAAG	zero	-0.0118771	0.0098778	0.9904083	-1.929049	1.942773	0.6644103	0.4306552
VEGFA	Model 5	hapCTACAAAGGAG	one	-0.4268931	0.0184136	0.8163281	-3.956419	3.23234	0.7390075	0.4306552
VEGFA	Model 5	hapCTACAAAGGAG	zero	0.2219231	0.0104756	0.8324531	-1.814842	2.300939	0.7390075	0.4306552
VEGFA	Model 5	hapCTACGGGAAA	one	1.460608	0.0350194	0.6789129	-5.269706	8.669092	0.6709212	0.4306552
VEGFA	Model 5	hapCTACGGGAAA	zero	-0.0419886	0.0098105	0.9658628	-1.945648	1.898629	0.6709212	0.4306552
VEGFA	Model 5	hapCTGACGAAAG	one	-0.4273981	0.0173651	0.8052287	-3.759335	3.019893	0.7194883	0.4306552
VEGFA	Model 5	hapCTGACGAAAG	zero	0.2500776	0.0107377	0.8161145	-1.837684	2.382243	0.7194883	0.4306552
ACE	Model 5	hapACCAGAGGAAAGATGGG	one	-0.2629446	0.02828	0.9258418	-5.64074	5.421346	0.8223886	0.4379879
ACE	Model 5	hapACCAGAGGAAAGATGGG	zero	-0.9179996	0.0135692	0.4968783	-3.518359	1.752444	0.8223886	0.4379879
ACE	Model 5	hapTGCAGAGAAAAGGAAGA	one	-1.680454	0.049735	0.7333615	-10.81222	8.386292	0.8609323	0.4379879
ACE	Model 5	hapTGCAGAGAAAAGGAAGA	zero	-0.798529	0.0133291	0.547649	-3.356563	1.827213	0.8609323	0.4379879
ACE	Model 5	hapTGCAGAGGAAAGGGAAAAGA	one	-0.0070263	0.0403503	0.9986109	-7.610373	8.222049	0.8250117	0.4379879
ACE	Model 5	hapTGCAGAGGAAAGGGAAAAGA	zero	-0.9085187	0.0132047	0.4896199	-3.440183	1.689523	0.8250117	0.4379879
ACE	Model 5	hapTGCAGAGGAAAGGGAGAAGA	one	-0.7928264	0.0150474	0.5969322	-3.675949	2.176592	0.8978751	0.4379879
ACE	Model 5	hapTGCAGAGGAAAGGGAGAAGA	zero	-1.028265	0.0165034	0.5312706	-4.178397	2.225428	0.8978751	0.4379879
AGT	Model 5	hapGGGCAGGGA	one	-0.1058168	0.0180087	0.9531312	-3.570216	3.483047	0.8805913	0.4379879
AGT	Model 5	hapGGGCAGGGA	zero	0.19739	0.0109887	0.857618	-1.937526	2.378785	0.8805913	0.4379879
AGTR1	Model 5	hapAAGAAAGAATCGGGG	one	-0.6449134	0.0380448	0.8649949	-7.783991	7.04685	0.8312814	0.4379879
AGTR1	Model 5	hapAAGAAAGAATCGGGG	zero	0.1791878	0.0099409	0.857117	-1.753791	2.150198	0.8312814	0.4379879
AGTR1	Model 5	hapAAGGAGGGGAGAAGA	one	-0.0277979	0.0128298	0.9827158	-2.510356	2.517978	0.8703032	0.4379879
AGTR1	Model 5	hapAAGGAGGGGAGAAGA	zero	0.2064633	0.0114325	0.8568694	-2.013919	2.47716	0.8703032	0.4379879
AGTR1	Model 5	hapwaste	one	0.1476596	0.0097314	0.8795143	-1.744368	2.076121	0.8869843	0.4379879
AGTR1	Model 5	hapwaste	zero	0.3114778	0.0153478	0.8394649	-2.661072	3.374803	0.8869843	0.4379879
ALOX15	Model 5	hapAAAGAACGAGA	one	-0.3354644	0.02638	0.8986655	-5.357563	4.953126	0.8610713	0.4379879
ALOX15	Model 5	hapAAAGAACGAGA	zero	0.1482859	0.0102411	0.8849866	-1.841868	2.178791	0.8610713	0.4379879
ALOX15	Model 5	hapAAAGAACGAG	one	0.6236114	0.0262454	0.8128062	-4.421595	5.935134	0.8378768	0.4379879
ALOX15	Model 5	hapAAAGAACGAG	zero	0.0700901	0.0100819	0.9446084	-1.8879	2.067155	0.8378768	0.4379879
ALOX15	Model 5	hapwaste	one	0.2805466	0.0115427	0.8082787	-1.962651	2.57507	0.7750307	0.4379879
ALOX15	Model 5	hapwaste	zero	-0.0921498	0.0118766	0.938142	-2.390924	2.260762	0.7750307	0.4379879
PTGS1	Model 5	hapwaste	one	0.1641582	0.0111037	0.8825935	-1.992146	2.367904	0.7958922	0.4379879
PTGS1	Model 5	hapwaste	zero	-0.1496222	0.011873	0.8996673	-2.446369	2.201198	0.7958922	0.4379879

gene	analysis	haplotype	num_haplos	estimate	stder	p	min95	max95	p_int	q
TLR4	Model 5	hapAGAGAGGGAG	one	-0.3122743	0.0193356	0.8715316	-4.019459	3.538098	0.7954132	0.4379879
TLR4	Model 5	hapAGAGAGGGAG	zero	0.2317886	0.0106737	0.8283243	-1.843278	2.350723	0.7954132	0.4379879
TLR4	Model 5	hapGAGGCGGCAA	one	-0.0220009	0.0171375	0.9897586	-3.324378	3.393183	0.9119198	0.4394794
TLR4	Model 5	hapGAGGCGGCAA	zero	0.1787174	0.010536	0.8654587	-1.868786	2.268941	0.9119198	0.4394794
ALOX15	Model 5	hapAAAAAGGCAG	one	0.4327026	0.030433	0.8872073	-5.38271	6.605545	0.9608039	0.4468855
ALOX15	Model 5	hapAAAAAGGCAG	zero	0.2793013	0.0100265	0.780935	-1.672101	2.269431	0.9608039	0.4468855
VEGFA	Model 5	hapCTACAAAGAAG	one	0.3112489	0.0257959	0.9041345	-4.634323	5.513293	0.9513001	0.4468855
VEGFA	Model 5	hapCTACAAAGAAG	zero	0.1497171	0.0100669	0.8818913	-1.806955	2.145379	0.9513001	0.4468855
VEGFA	Model 5	hapCTGACGGAAGG	one	-0.0349833	0.0232009	0.9879705	-4.478873	4.615648	0.9415799	0.4468855
VEGFA	Model 5	hapCTGACGGAAGG	zero	0.1386537	0.0100803	0.8906993	-1.820363	2.13676	0.9415799	0.4468855
AGTR1	Model 3	hapGCAGGGGGTCGAGG	one	7.264874	0.0271057	0.0098131	1.715022	13.11754	0.0069477	0.4724436
AGTR1	Model 3	hapGCAGGGGGTCGAGG	zero	-0.6215961	0.0107891	0.5634423	-2.701021	1.502269	0.0069477	0.4724436
AGTR1	Model 1	hapGCAGGGGGTCGAGG	one	7.851636	0.0289402	0.0091416	1.904365	14.146	0.0069465	0.49257
AGTR1	Model 1	hapGCAGGGGGTCGAGG	zero	-0.5575882	0.0108057	0.6049526	-2.641516	1.570946	0.0069465	0.49257
ACE	Model 2	hapACCAGAGGAAAGAAAAGA	one	-3.613334	0.0233078	0.1146591	-7.917444	0.8919584	0.197949	0.5944913
ACE	Model 2	hapACCAGAGGAAAGAAAAGA	zero	-0.2508827	0.0160975	0.8760267	-3.348884	2.946421	0.197949	0.5944913
ACE	Model 2	hapTGCAGAGGAAAGGGAGTGG	one	2.71378	0.0436345	0.5395901	-5.705379	11.88465	0.3943835	0.5944913
ACE	Model 2	hapTGCAGAGGAAAGGGAGTGG	zero	-1.100743	0.0147889	0.4543763	-3.926257	1.807868	0.3943835	0.5944913
ACE	Model 2	hapTGCAGAGGAAAGGGAGTGG	one	-5.040721	0.0340698	0.1293011	-11.17461	1.516744	0.183811	0.5944913
ACE	Model 2	hapTGCAGAGGAAAGGGAGTGG	zero	-0.4283048	0.0151337	0.776759	-3.338377	2.569377	0.183811	0.5944913
ADRB2	Model 2	hapAGAC	one	1.321216	0.0124192	0.2908227	-1.115298	3.817765	0.0464803	0.5944913
ADRB2	Model 2	hapAGAC	zero	-1.599776	0.0130987	0.2185396	-4.093855	0.9591631	0.0464803	0.5944913
ADRB2	Model 2	hapAGAG	one	-3.067716	0.0321398	0.3325616	-8.985415	3.234748	0.3021009	0.5944913
ADRB2	Model 2	hapAGAG	zero	0.311254	0.0108074	0.7737482	-1.791204	2.458721	0.3021009	0.5944913
ADRB2	Model 2	hapGCGC	one	0.6892497	0.0133358	0.6066192	-1.908438	3.35573	0.3781579	0.5944913
ADRB2	Model 2	hapGCGC	zero	-0.6709534	0.0126884	0.5958326	-3.110693	1.83022	0.3781579	0.5944913
ADRB2	Model 2	hapGGAC	one	-2.632155	0.0171508	0.1201978	-5.850764	0.6964867	0.0511101	0.5944913
ADRB2	Model 2	hapGGAC	zero	0.8986039	0.0114365	0.4342685	-1.337892	3.185797	0.0511101	0.5944913
AGT	Model 2	hapAAGCGAAGA	one	-0.5752822	0.0120957	0.6334791	-2.904636	1.809954	0.4359603	0.5944913
AGT	Model 2	hapAAGCGAAGA	zero	0.5192264	0.0131702	0.6942393	-2.042292	3.147727	0.4359603	0.5944913
AGT	Model 2	hapAGAAGGGGA	one	1.046606	0.0159818	0.5148935	-2.0695	4.261866	0.3556643	0.5944913
AGT	Model 2	hapAGAAGGGGA	zero	-0.6033113	0.0119036	0.6113081	-2.89545	1.742933	0.3556643	0.5944913
AGT	Model 2	hapwaste	one	1.386709	0.0190485	0.4698577	-2.328717	5.24347	0.3486986	0.5944913
AGT	Model 2	hapwaste	zero	-0.5228768	0.0113428	0.6440495	-2.710005	1.71342	0.3486986	0.5944913
AGTR1	Model 2	hapAAGAAAAAAAGAAGA	one	-4.11386	0.0335929	0.2114018	-10.22375	2.411848	0.1924998	0.5944913
AGTR1	Model 2	hapAAGAAAAAAAGAAGA	zero	0.2305706	0.0106387	0.828659	-1.837747	2.342468	0.1924998	0.5944913
AGTR1	Model 2	hapAAGGAGGGAGAAGG	one	-2.168673	0.0260516	0.4002077	-7.038581	2.956353	0.3662495	0.5944913
AGTR1	Model 2	hapAAGGAGGGAGAAGG	zero	0.2221457	0.0107986	0.8372321	-1.876754	2.365942	0.3662495	0.5944913
ALOX15	Model 2	hapAAAGAACAAAGA	one	2.649529	0.0217424	0.2293644	-1.632922	7.118419	0.1593318	0.5944913
ALOX15	Model 2	hapAAAGAACAAAGA	zero	-0.6641065	0.0112603	0.5541576	-2.832421	1.552595	0.1593318	0.5944913
ALOX15	Model 2	hapAAGAACGCAGA	one	-0.9191143	0.0135001	0.494155	-3.506392	1.737536	0.3422175	0.5944913
ALOX15	Model 2	hapAAGAACGCAGA	zero	0.5897717	0.0127724	0.6453302	-1.897077	3.139661	0.3422175	0.5944913
ALOX15	Model 2	hapTAAAAGGCAG	one	4.754138	0.0341748	0.1744325	-2.032614	12.01105	0.1446462	0.5944913
ALOX15	Model 2	hapTAAAAGGCAG	zero	-0.5003554	0.0108271	0.6432561	-2.589566	1.633664	0.1446462	0.5944913
EDN1	Model 2	hapAGAC	one	-0.603151	0.0105885	0.567889	-2.644684	1.481193	0.0768585	0.5944913
EDN1	Model 2	hapAGAC	zero	1.671556	0.0151121	0.2729223	-1.295707	4.728021	0.0768585	0.5944913
EDN1	Model 2	hapCAGA	one	1.185681	0.0175064	0.5009124	-2.227309	4.71781	0.3356549	0.5944913
EDN1	Model 2	hapCAGA	zero	-0.7028589	0.0118089	0.550445	-2.974698	1.622175	0.3356549	0.5944913

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
EDN1	Model 2	hapwaste	one	-3.983636	0.0399378	0.3089855	-11.21284	3.834186	0.3054706	0.5944913
EDN1	Model 2	hapwaste	zero	0.1301513	0.0107448	0.9036753	-1.956486	2.261198	0.3054706	0.5944913
GRK4	Model 2	hapACAGGAGCAAGAAGAGAAAG	one	1.011146	0.0167182	0.5474583	-2.245063	4.375819	0.4227729	0.5944913
GRK4	Model 2	hapACAGGAGCAAGAAGAGAAAG	zero	-0.4385463	0.0115166	0.7028153	-2.660686	1.834322	0.4227729	0.5944913
GRK4	Model 2	hapACAGGAGCAAGAAGGGAAAG	one	2.046829	0.024675	0.4117626	-2.770933	7.103315	0.3429347	0.5944913
GRK4	Model 2	hapACAGGAGCAAGAAGGGAAAG	zero	-0.3952814	0.0109235	0.7169957	-2.505123	1.760219	0.3429347	0.5944913
GRK4	Model 2	hapACGGGAACAAAACAGACGA	one	-3.156159	0.0296117	0.2790563	-8.616776	2.630757	0.2622096	0.5944913
GRK4	Model 2	hapACGGGAACAAAACAGACGA	zero	0.2313126	0.0108716	0.831744	-1.881827	2.389962	0.2622096	0.5944913
GRK4	Model 2	hapTGGAGTAAGGAACAAGAAG	one	-2.443215	0.0260734	0.3430076	-7.303402	2.671798	0.3197371	0.5944913
GRK4	Model 2	hapTGGAGTAAGGAACAAGAAG	zero	0.2388274	0.0109848	0.8281297	-1.896222	2.420342	0.3197371	0.5944913
GRK4	Model 2	hapTGGAGTAAGGAACAGGAAG	one	-1.987321	0.0172233	0.2441046	-5.240715	1.377773	0.2059626	0.5944913
GRK4	Model 2	hapTGGAGTAAGGAACAGGAAG	zero	0.3550032	0.0115266	0.7585717	-1.886767	2.647995	0.2059626	0.5944913
GRK4	Model 2	hapwaste	one	0.5758009	0.0134913	0.6705133	-2.048821	3.27075	0.4297882	0.5944913
GRK4	Model 2	hapwaste	zero	-0.597986	0.0122365	0.6241308	-2.953597	1.814803	0.4297882	0.5944913
PTGS1	Model 2	hapGAGAGGGGCAG	one	0.7466137	0.0132012	0.5732467	-1.826666	3.387344	0.3290686	0.5944913
PTGS1	Model 2	hapGAGAGGGGCAG	zero	-0.7087585	0.0125301	0.5703955	-3.117514	1.759885	0.3290686	0.5944913
PTGS1	Model 2	hapGGGAGGGCAGG	one	-3.150224	0.0247461	0.1961372	-7.735487	1.662912	0.1601153	0.5944913
PTGS1	Model 2	hapGGGAGGGCAGG	zero	0.355458	0.0108506	0.7437282	-1.756253	2.512559	0.1601153	0.5944913
PTGS1	Model 2	hapGGGAGGGGCAG	one	0.5947808	0.0123447	0.6310604	-1.80992	3.058374	0.3664477	0.5944913
PTGS1	Model 2	hapGGGAGGGGCAG	zero	-0.7390253	0.0132792	0.5765648	-3.289146	1.878338	0.3664477	0.5944913
PTGS1	Model 2	hapGGGGGAGCAGA	one	-4.29144	0.0538804	0.4157989	-13.88324	6.368706	0.4095273	0.5944913
PTGS1	Model 2	hapGGGGGAGCAGA	zero	0.0861151	0.0104756	0.9345282	-1.947886	2.16231	0.4095273	0.5944913
PTGS1	Model 2	hapGGGGGGGGCAG	one	-2.312207	0.0194547	0.2294691	-5.966971	1.484607	0.1750939	0.5944913
PTGS1	Model 2	hapGGGGGGGGCAG	zero	0.5310236	0.0114962	0.6451209	-1.708823	2.821911	0.1750939	0.5944913
PTGS2	Model 2	hapAGC	one	1.588518	0.0211501	0.4563467	-2.536582	5.888211	0.3536029	0.5944913
PTGS2	Model 2	hapAGC	zero	-0.5059884	0.0112635	0.6525438	-2.678365	1.71488	0.3536029	0.5944913
TLR4	Model 2	hapAAGGCCCAA	one	-1.754671	0.0178541	0.3216785	-5.133154	1.74413	0.2649518	0.5944913
TLR4	Model 2	hapAAGGCCCAA	zero	0.5045565	0.0120255	0.67556591	-1.836591	2.90154	0.2649518	0.5944913
TLR4	Model 2	hapAGAAAGCAA	one	2.043368	0.0192407	0.2933769	-1.733145	5.965017	0.2049895	0.5944913
TLR4	Model 2	hapAGAAAGCAA	zero	-0.5900108	0.01136	0.6025431	-2.778939	1.648201	0.2049895	0.5944913
TLR4	Model 2	hapAGAAAGCGGG	one	-2.789819	0.0246819	0.2519137	-7.380483	2.02838	0.2145946	0.5944913
TLR4	Model 2	hapAGAAAGCGGG	zero	0.3227219	0.0108709	0.7669953	-1.79221	2.483199	0.2145946	0.5944913
TLR4	Model 2	hapAGAGAGGCAA	one	2.842962	0.0360407	0.4368626	-4.171064	10.37037	0.3963583	0.5944913
TLR4	Model 2	hapAGAGAGGCAA	zero	-0.313872	0.010721	0.7694114	-2.386696	1.802969	0.3963583	0.5944913
TLR4	Model 2	hapAGAGAGGCGG	one	2.084803	0.0274139	0.4518249	-3.255493	7.719884	0.384226	0.5944913
TLR4	Model 2	hapAGAGAGGCGG	zero	-0.2937891	0.0106279	0.7819604	-2.349209	1.804895	0.384226	0.5944913
VEGFA	Model 2	hapAAACAAAGGAG	one	2.458946	0.0245875	0.3234012	-2.361531	7.517413	0.2574471	0.5944913
VEGFA	Model 2	hapAAACAAAGGAG	zero	-0.4259775	0.0108679	0.6945533	-2.52454	1.717766	0.2574471	0.5944913
VEGFA	Model 2	hapCTAACGAAAG	one	2.779944	0.0312286	0.3801326	-3.322257	9.267309	0.3170547	0.5944913
VEGFA	Model 2	hapCTAACGAAAG	zero	-0.4234172	0.0106474	0.6903357	-2.479905	1.676437	0.3170547	0.5944913
VEGFA	Model 2	hapCTACAAAGAAAG	one	-2.195073	0.0263898	0.4005199	-7.125246	2.996813	0.3837984	0.5944913
VEGFA	Model 2	hapCTACAAAGAAAG	zero	0.1551222	0.0108801	0.8867427	-1.958039	2.31383	0.3837984	0.5944913
VEGFA	Model 2	hapCTACAAAGGAG	one	-1.586188	0.0198597	0.4209536	-5.343277	2.320025	0.3801307	0.5944913
VEGFA	Model 2	hapCTACAAAGGAG	zero	0.2428341	0.0112089	0.828735	-1.935394	2.469445	0.3801307	0.5944913
VEGFA	Model 2	hapCTACAAAGGG	one	-3.591085	0.0299704	0.222657	-9.091114	2.241699	0.2027291	0.5944913
VEGFA	Model 2	hapCTACAAAGGG	zero	0.2316761	0.0107205	0.8291442	-1.852399	2.360004	0.2027291	0.5944913
VEGFA	Model 2	hapCTACCAGAGAA	one	-2.380923	0.0301108	0.4237356	-7.975316	3.553565	0.4155993	0.5944913
VEGFA	Model 2	hapCTACCAGAGAA	zero	0.0945475	0.0107542	0.9299932	-1.993141	2.226707	0.4155993	0.5944913

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
VEGFA	Model 2	hapCTACCGAGAAG	one	2.28375	0.0170114	0.1846855	-1.070337	5.751554	0.0851807	0.5944913
VEGFA	Model 2	hapCTACCGAGAAG	zero	-1.024958	0.0118538	0.3849869	-3.297942	1.301454	0.0851807	0.5944913
VEGFA	Model 2	hapCTGACGGAAAA	one	-3.855671	0.0288012	0.1724944	-9.13261	1.727715	0.1695497	0.5944913
VEGFA	Model 2	hapCTGACGGAAAA	zero	0.1602887	0.0108187	0.882341	-1.94118	2.306793	0.1695497	0.5944913
EDN1	Model 2	hapAGGC	one	0.2323047	0.0115403	0.8406889	-2.009365	2.525255	0.4514915	0.6019887
EDN1	Model 2	hapAGGC	zero	-0.7582471	0.0133662	0.5691809	-3.324358	1.875977	0.4514915	0.6019887
AGTR1	Model 2	hapAAGAAGGGGAGAAGA	one	0.9142026	0.0172779	0.5985092	-2.445939	4.39008	0.4913351	0.6408719
AGTR1	Model 2	hapAAGAAGGGGAGAAGA	zero	-0.3842619	0.0115746	0.7394863	-2.618687	1.901432	0.4913351	0.6408719
ACE	Model 2	hapACCAGGAAGGGAGAAGA	one	-2.504087	0.0360481	0.4819099	-9.154746	4.633459	0.587027	0.644654
ACE	Model 2	hapACCAGGAAGGGAGAAGA	zero	-0.5730562	0.0147063	0.6960371	-3.398008	2.334506	0.587027	0.644654
ACE	Model 2	hapwaste	one	-0.7047383	0.0151012	0.6396521	-3.600599	2.278115	0.5261432	0.644654
ACE	Model 2	hapwaste	zero	-1.857673	0.0182864	0.3054075	-5.312869	1.723604	0.5261432	0.644654
ADRB2	Model 2	hapGGGG	one	-0.4335499	0.0118261	0.7133966	-2.714825	1.90122	0.556793	0.644654
ADRB2	Model 2	hapGGGG	zero	0.3805157	0.0133937	0.7768048	-2.220296	3.050506	0.556793	0.644654
AGT	Model 2	hapAGGCAGGGA	one	-0.7694475	0.0222652	0.728725	-5.006643	3.656749	0.7303899	0.644654
AGT	Model 2	hapAGGCAGGGA	zero	0.0261176	0.0110696	0.9811835	-2.120669	2.21999	0.7303899	0.644654
AGT	Model 2	hapGGGCAGGAG	one	-0.8329901	0.0218652	0.7021261	-4.993016	3.509189	0.7120082	0.644654
AGT	Model 2	hapGGGCAGGAG	zero	0.0158697	0.0111827	0.9886811	-2.152404	2.232192	0.7120082	0.644654
AGT	Model 2	hapGGGCAGGGA	one	-0.9408898	0.0199733	0.6360993	-4.743824	3.013869	0.5987275	0.644654
AGT	Model 2	hapGGGCAGGGA	zero	0.2146688	0.0115726	0.8530331	-2.032813	2.51371	0.5987275	0.644654
AGTR1	Model 2	hapAAGGAGGGGAGAAGA	one	-0.4502527	0.0135737	0.7396123	-3.063746	2.233703	0.6925967	0.644654
AGTR1	Model 2	hapAAGGAGGGGAGAAGA	zero	0.1518942	0.0123492	0.9022064	-2.243082	2.605545	0.6925967	0.644654
ALOX15	Model 2	hapAAAAAGGGCAG	one	2.232753	0.0343975	0.5210448	-4.432364	9.362711	0.512971	0.644654
ALOX15	Model 2	hapAAAAAGGGCAG	zero	-0.0909368	0.0107536	0.9325944	-2.174652	2.037163	0.512971	0.644654
ALOX15	Model 2	hapAAAGAACGAGA	one	-1.730515	0.0308995	0.5722362	-7.505281	4.40479	0.5787074	0.644654
ALOX15	Model 2	hapAAAGAACGAGA	zero	0.0548805	0.0109897	0.9601927	-2.0772	2.233383	0.5787074	0.644654
ALOX15	Model 2	hapAAAGAGGCAG	one	-1.448202	0.0301971	0.6291382	-7.111761	4.560675	0.6292815	0.644654
ALOX15	Model 2	hapAAAGAGGCAG	zero	0.0045728	0.0106335	0.9965697	-2.058073	2.110658	0.6292815	0.644654
ALOX15	Model 2	hapAAAGGACAAGA	one	1.174872	0.0384846	0.7615687	-6.17587	9.101516	0.7247398	0.644654
ALOX15	Model 2	hapAAAGGACAAGA	zero	-0.2061851	0.0106424	0.8462629	-2.266197	1.897248	0.7247398	0.644654
ALOX15	Model 2	hapAGAGAGGCAG	one	-1.525359	0.0302794	0.611816	-7.199453	4.495667	0.6171607	0.644654
ALOX15	Model 2	hapAGAGAGGCAG	zero	-0.0051299	0.010681	0.9961687	-2.076696	2.11026	0.6171607	0.644654
ALOX15	Model 2	hapwaste	one	-0.4294066	0.0125829	0.7324245	-2.854979	2.056729	0.6584206	0.644654
ALOX15	Model 2	hapwaste	zero	0.1868473	0.0125745	0.8820151	-2.252142	2.686694	0.6584206	0.644654
EDN1	Model 2	hapAAGA	one	1.381354	0.0251166	0.5850422	-3.488562	6.497003	0.5264828	0.644654
EDN1	Model 2	hapAAGA	zero	-0.3059526	0.0111061	0.7826789	-2.452599	1.887933	0.5264828	0.644654
EDN1	Model 2	hapCGC	one	1.204659	0.0372047	0.7476285	-5.912535	8.860229	0.7215352	0.644654
EDN1	Model 2	hapCGC	zero	-0.1531043	0.0107166	0.8863379	-2.228429	1.966272	0.7215352	0.644654
PTGS1	Model 2	hapGGGGAGGCAG	one	-1.167559	0.0305365	0.7006174	-6.909197	4.928211	0.7262939	0.644654
PTGS1	Model 2	hapGGGGAGGCAG	zero	-0.082388	0.0107339	0.9388086	-2.1625	2.041949	0.7262939	0.644654
PTGS2	Model 2	hapCGA	one	0.6042313	0.0157407	0.7020154	-2.452136	3.756361	0.5557004	0.644654
PTGS2	Model 2	hapCGA	zero	1.643902	0.0310153	0.5991997	-4.350865	8.014388	0.5557004	0.644654
TLR4	Model 2	hapAAGGCAGCAA	one	0.3202553	0.0118685	0.787674	-1.986449	2.681247	0.5723838	0.644654
TLR4	Model 2	hapAAGGCAGCAA	zero	-0.5125726	0.0137609	0.7088989	-3.159978	2.207207	0.5723838	0.644654
TLR4	Model 2	hapAGAGAGGGAG	one	0.629356	0.0210502	0.7657331	-3.437889	4.867916	0.6850092	0.644654
TLR4	Model 2	hapAGAGAGGGAG	zero	-0.2875963	0.0113074	0.798999	-2.473118	1.946901	0.6850092	0.644654
TLR4	Model 2	hapwaste	one	-0.7021391	0.0173543	0.6848168	-4.022844	2.733459	0.6231237	0.644654
TLR4	Model 2	hapwaste	zero	0.1844372	0.0112948	0.8704388	-2.009022	2.426996	0.6231237	0.644654

gene	analysis	haplotype	num_haplos	estimate	stder	p	min95	max95	p_int	q
VEGFA	Model 2	hapCTGACGGAAAG	one	-0.7208891	0.0184235	0.6946213	-4.241846	2.929531	0.6992638	0.644654
VEGFA	Model 2	hapCTGACGGAAAG	zero	0.0529577	0.0115604	0.9634808	-2.188545	2.345829	0.6992638	0.644654
VEGFA	Model 2	hapwaste	one	-0.2312122	0.0115912	0.8417534	-2.472238	2.061309	0.7306079	0.644654
VEGFA	Model 2	hapwaste	zero	0.2145747	0.0131563	0.8706126	-2.336504	2.83229	0.7306079	0.644654
ACE	Model 2	hapTGCAGAGAAGGGAAAAGA	one	0.0353725	0.0389107	0.9927499	-7.310021	7.962865	0.8061019	0.6452875
ACE	Model 2	hapTGCAGAGAAGGGAAAAGA	zero	-0.9216342	0.0147069	0.5291185	-3.736804	1.975864	0.8061019	0.6452875
ACE	Model 2	hapTGCAGAGAAGGGAGAAGA	one	-0.7202806	0.0160146	0.6518049	-3.78808	2.445338	0.8613381	0.6452875
ACE	Model 2	hapTGCAGAGAAGGGAGAAGA	zero	-1.062328	0.0185301	0.5644971	-4.591103	2.596961	0.8613381	0.6452875
ADRB2	Model 2	hapwaste	one	0.5570449	0.0295019	0.8506854	-5.092515	6.542906	0.8189566	0.6452875
ADRB2	Model 2	hapwaste	zero	-0.1331621	0.010745	0.9013308	-2.214349	1.992319	0.8189566	0.6452875
AGT	Model 2	hapAGGAGGGAG	one	0.2058643	0.0145301	0.8874756	-2.607598	3.100601	0.8275686	0.6452875
AGT	Model 2	hapAGGAGGGAG	zero	-0.157672	0.0122225	0.897302	-2.521042	2.262998	0.8275686	0.6452875
AGTR1	Model 2	hapwaste	one	-0.0783138	0.0104508	0.9402577	-2.104216	1.989514	0.8216756	0.6452875
AGTR1	Model 2	hapwaste	zero	-0.3560715	0.0164403	0.828275	-3.515656	2.906981	0.8216756	0.6452875
ALOX15	Model 2	hapAAAGAACGAGG	one	0.1319326	0.0153318	0.9314877	-2.832252	3.186542	0.8711381	0.6452875
ALOX15	Model 2	hapAAAGAACGAGG	zero	-0.1440412	0.0119483	0.904	-2.455324	2.222007	0.8711381	0.6452875
ALOX15	Model 2	hapAAAGAACGAG	one	-0.6406937	0.027327	0.814095	-5.822369	4.826078	0.8364657	0.6452875
ALOX15	Model 2	hapAAAGAACGAG	zero	-0.0634142	0.0108229	0.9532734	-2.160989	2.07913	0.8364657	0.6452875
GRK4	Model 2	hapACAGGAGCAAGAAGGACGA	one	-0.5560662	0.0197701	0.7779629	-4.33569	3.372887	0.7711012	0.6452875
GRK4	Model 2	hapACAGGAGCAAGAAGGACGA	zero	0.0545206	0.0113126	0.9615813	-2.139503	2.297734	0.7711012	0.6452875
PTGS1	Model 2	hapwaste	one	-0.0802539	0.0118867	0.9461629	-2.381218	2.274946	0.8523337	0.6452875
PTGS1	Model 2	hapwaste	zero	-0.3183933	0.0126965	0.8017319	-2.768323	2.193267	0.8523337	0.6452875
PTGS2	Model 2	hapCAA	one	-1.052375	0.0406315	0.7946268	-8.626609	7.149711	0.805065	0.6452875
PTGS2	Model 2	hapCAA	zero	-0.0244117	0.0108044	0.9819763	-2.119266	2.115277	0.805065	0.6452875
PTGS2	Model 2	hapwaste	one	0.4299799	0.0309835	0.8898895	-5.487307	6.717739	0.861428	0.6452875
PTGS2	Model 2	hapwaste	zero	-0.1281018	0.0108377	0.9058731	-2.227165	2.016026	0.861428	0.6452875
TLR4	Model 2	hapGAGGCGGCAA	one	-0.5216056	0.0180556	0.7721479	-3.980411	3.061792	0.7456428	0.6452875
TLR4	Model 2	hapGAGGCGGCAA	zero	0.0988088	0.0113598	0.930738	-2.105239	2.35248	0.7456428	0.6452875
VEGFA	Model 2	hapCTACCGGGAAA	one	0.9668843	0.0394242	0.8072241	-6.541022	9.077929	0.7570744	0.6452875
VEGFA	Model 2	hapCTACCGGGAAA	zero	-0.2565083	0.0104987	0.806787	-2.287962	1.81718	0.7570744	0.6452875
ACE	Model 2	hapACCAGAGGAAAGATGGG	one	-0.5308985	0.0291499	0.8551396	-6.054555	5.317529	0.9120036	0.6592797
ACE	Model 2	hapACCAGAGGAAAGATGGG	zero	-0.8631982	0.0151404	0.5670416	-3.761825	2.122733	0.9120036	0.6592797
GRK4	Model 2	hapACAGGAGCAAGAACGAG	one	-0.0359424	0.012339	0.9767632	-2.424471	2.411055	0.9061002	0.6592797
GRK4	Model 2	hapACAGGAGCAAGAACGAG	zero	-0.2057224	0.0130599	0.8747376	-2.727737	2.381682	0.9061002	0.6592797
VEGFA	Model 2	hapCTGACGGAAGG	one	-0.2667741	0.0236439	0.9100683	-4.783069	4.463736	0.9375995	0.6697139
VEGFA	Model 2	hapCTGACGGAAGG	zero	-0.0780482	0.0108405	0.9425964	-2.178689	2.067702	0.9375995	0.6697139
ACE	Model 1	hapACCAGAGGAAAGAAAGA	one	-3.397787	0.0243306	0.1556924	-7.896359	1.320506	0.2098966	0.6762411
ACE	Model 1	hapACCAGAGGAAAGAAAGA	zero	0.0056705	0.0159973	0.9971726	-3.081278	3.190942	0.2098966	0.6762411
ACE	Model 1	hapTGCAGAGAAGGGAGTGG	one	3.329376	0.0426322	0.4425296	-4.953701	12.33431	0.3410417	0.6762411
ACE	Model 1	hapTGCAGAGAAGGGAGTGG	zero	-0.8742614	0.0147601	0.5520334	-3.700817	2.035259	0.3410417	0.6762411
ACE	Model 1	hapTGCAGAGAAGGGAGTGG	one	-5.264436	0.0335645	0.1074419	-11.29606	1.177324	0.1331165	0.6762411
ACE	Model 1	hapTGCAGAGAAGGGAGTGG	zero	-0.1200934	0.0150616	0.936426	-3.025474	2.872333	0.1331165	0.6762411
ACE	Model 1	hapwaste	one	-0.4136353	0.0150321	0.782806	-3.304887	2.564067	0.4421157	0.6762411
ACE	Model 1	hapwaste	zero	-1.801235	0.0180606	0.3144581	-5.216486	1.737076	0.4421157	0.6762411
ADRB2	Model 1	hapAGAC	one	1.38065	0.0125166	0.2735588	-1.076176	3.898494	0.0464147	0.6762411
ADRB2	Model 1	hapAGAC	zero	-1.578207	0.013128	0.2258927	-4.078338	0.9870881	0.0464147	0.6762411
ADRB2	Model 1	hapAGAG	one	-3.406807	0.0321981	0.2819549	-9.314169	2.885366	0.246018	0.6762411
ADRB2	Model 1	hapAGAG	zero	0.4062379	0.0108521	0.7087936	-1.706816	2.564717	0.246018	0.6762411

gene	analysis	haplotype	num_haplos	estimate	stder	p	min95	max95	p_int	q
ADRB2	Model 1	hapGCAC	one	0.7130881	0.0134475	0.5973448	-1.906702	3.402845	0.3939981	0.6762411
ADRB2	Model 1	hapGCGC	zero	-0.6035165	0.0126149	0.6314286	-3.030938	1.884671	0.3939981	0.6762411
ADRB2	Model 1	hapGGAC	one	-2.466517	0.0170783	0.1439594	-5.677201	0.8534554	0.0626204	0.6762411
ADRB2	Model 1	hapGGAC	zero	0.9076902	0.0114907	0.4318348	-1.339479	3.206043	0.0626204	0.6762411
AGT	Model 1	hapAAGCGAAGA	one	-0.5674997	0.0121103	0.638497	-2.89981	1.820832	0.3903383	0.6762411
AGT	Model 1	hapAAGCGAAGA	zero	0.6492109	0.0132296	0.6248494	-1.927027	3.293123	0.3903383	0.6762411
AGT	Model 1	hapAGAAGGGGA	one	1.110662	0.0159965	0.4900466	-2.010229	4.330951	0.3490392	0.6762411
AGT	Model 1	hapAGAAGGGGA	zero	-0.5688067	0.0119329	0.6327325	-2.867326	1.784104	0.3490392	0.6762411
AGT	Model 1	hapwaste	one	1.450469	0.018902	0.44633	-2.239229	5.279423	0.3416993	0.6762411
AGT	Model 1	hapwaste	zero	-0.4781066	0.0113805	0.6737593	-2.673402	1.766706	0.3416993	0.6762411
AGTR1	Model 1	hapAAGAAAAAAAGAAGA	one	-3.499116	0.0329696	0.2802569	-9.537725	2.942587	0.2516408	0.6762411
AGTR1	Model 1	hapAAGAAAAAAAGAAGA	zero	0.250926	0.0106286	0.8136442	-1.815868	2.361226	0.2516408	0.6762411
AGTR1	Model 1	hapAAGAAGGGGAGAAGA	one	1.084074	0.0173105	0.5335032	-2.287967	4.572485	0.4482265	0.6762411
AGTR1	Model 1	hapAAGAAGGGGAGAAGA	zero	-0.349083	0.0115678	0.7624873	-2.582999	1.93606	0.4482265	0.6762411
AGTR1	Model 1	hapAAGGAGGGGAGAAGG	one	-2.324712	0.0259143	0.3642719	-7.16186	2.764466	0.3148581	0.6762411
AGTR1	Model 1	hapAAGGAGGGGAGAAGG	zero	0.3240649	0.0108213	0.7650146	-1.781348	2.474609	0.3148581	0.6762411
ALOX15	Model 1	hapAAAAAGGCAG	one	2.665926	0.0345146	0.446068	-4.049459	9.851309	0.4419124	0.6762411
ALOX15	Model 1	hapAAAAAGGCAG	zero	-0.0784798	0.0107747	0.9419276	-2.166497	2.054101	0.4419124	0.6762411
ALOX15	Model 1	hapAAAGAACAAAGA	one	2.812333	0.0215898	0.199216	-1.447432	7.25622	0.146001	0.6762411
ALOX15	Model 1	hapAAAGAACAAAGA	zero	-0.6000645	0.0113111	0.5947688	-2.779442	1.628168	0.146001	0.6762411
ALOX15	Model 1	hapAAGAACGCAGA	one	-0.8867821	0.0135954	0.5125054	-3.492924	1.789738	0.3156564	0.6762411
ALOX15	Model 1	hapAAGAACGCAGA	zero	0.7196018	0.0127749	0.5747337	-1.770932	3.273281	0.3156564	0.6762411
ALOX15	Model 1	hapTAAAAGGCAG	one	4.926301	0.0339904	0.1574523	-1.836119	12.15458	0.1353549	0.6762411
ALOX15	Model 1	hapTAAAAGGCAG	zero	-0.4382482	0.0108566	0.6858892	-2.534393	1.702977	0.1353549	0.6762411
EDN1	Model 1	hapAGAC	one	-0.6027086	0.0106068	0.5688412	-2.647742	1.485284	0.0593847	0.6762411
EDN1	Model 1	hapAGAC	zero	1.827787	0.0150995	0.2305943	-1.141607	4.886372	0.0593847	0.6762411
EDN1	Model 1	hapAGGC	one	0.3280039	0.0115512	0.7768585	-1.917896	2.62533	0.3781883	0.6762411
EDN1	Model 1	hapAGGC	zero	-0.8369251	0.0134032	0.5307707	-3.408002	1.802589	0.3781883	0.6762411
EDN1	Model 1	hapCAGA	one	1.339683	0.0173989	0.4445298	-2.057862	4.855086	0.2991268	0.6762411
EDN1	Model 1	hapCAGA	zero	-0.6937455	0.0118642	0.5574881	-2.976321	1.64253	0.2991268	0.6762411
EDN1	Model 1	hapwaste	one	-3.706081	0.0404345	0.3505397	-11.04282	4.235761	0.3421914	0.6762411
EDN1	Model 1	hapwaste	zero	0.1601167	0.0107408	0.8816199	-1.926373	2.290996	0.3421914	0.6762411
GRK4	Model 1	hapACAGGAGCAAGAAGGGAG	one	1.799981	0.02487	0.4733447	-3.043189	6.885077	0.4221286	0.6762411
GRK4	Model 1	hapACAGGAGCAAGAAGGGAG	zero	-0.2939127	0.0109692	0.7884952	-2.414647	1.872909	0.4221286	0.6762411
GRK4	Model 1	hapACGGGAACAAACAGACGA	one	-2.953243	0.0302671	0.3222059	-8.542852	2.977988	0.2968046	0.6762411
GRK4	Model 1	hapACGGGAACAAACAGACGA	zero	0.2692057	0.0108672	0.8046569	-1.843875	2.427776	0.2968046	0.6762411
GRK4	Model 1	hapTGGAGTAAGGAACAAGAAG	one	-2.508446	0.0262474	0.3333371	-7.396979	2.638154	0.2978539	0.6762411
GRK4	Model 1	hapTGGAGTAAGGAACAAGAAG	zero	0.3151898	0.0109823	0.7745192	-1.821015	2.497875	0.2978539	0.6762411
GRK4	Model 1	hapTGGAGTAAGGAACAGGAAG	one	-1.928796	0.0172027	0.2578333	-5.180301	1.434207	0.2074666	0.6762411
GRK4	Model 1	hapTGGAGTAAGGAACAGGAAG	zero	0.4120888	0.0115545	0.7219791	-1.836326	2.712003	0.2074666	0.6762411
GRK4	Model 1	hapwaste	one	0.7384963	0.013449	0.5844389	-1.882236	3.429229	0.3487837	0.6762411
GRK4	Model 1	hapwaste	zero	-0.6503257	0.0122639	0.5948389	-3.009903	1.766656	0.3487837	0.6762411
PTGS1	Model 1	hapGAGAGGGGCAG	one	0.7897873	0.0132367	0.5524336	-1.79143	3.438847	0.3426197	0.6762411
PTGS1	Model 1	hapGAGAGGGGCAG	zero	-0.6300015	0.0125418	0.6144344	-3.042877	1.842921	0.3426197	0.6762411
PTGS1	Model 1	hapGGGAGGGGCAGG	one	-2.97923	0.0249299	0.2253373	-7.605869	1.879088	0.1780385	0.6762411
PTGS1	Model 1	hapGGGAGGGGCAGG	zero	0.4105485	0.0108547	0.7059212	-1.703104	2.56965	0.1780385	0.6762411
PTGS1	Model 1	hapGGGAGGGGCAG	one	0.576483	0.0124098	0.643319	-1.840306	3.052776	0.4372593	0.6762411
PTGS1	Model 1	hapGGGAGGGGCAG	zero	-0.5813008	0.013304	0.6613286	-3.14018	2.04518	0.4372593	0.6762411

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
PTGS1	Model 1	hapGGGGGAGCAGA	one	-4.030259	0.0535361	0.4424306	-13.58995	6.587033	0.4285906	0.6762411
PTGS1	Model 1	hapGGGGGAGCAGA	zero	0.1464817	0.0104779	0.8889265	-1.889183	2.224384	0.4285906	0.6762411
PTGS1	Model 1	hapGGGGGGGGCAG	one	-2.533046	0.01943	0.1869791	-6.175001	1.250277	0.1238905	0.6762411
PTGS1	Model 1	hapGGGGGGGGCAG	zero	0.6945637	0.0115229	0.548187	-1.554084	2.994574	0.1238905	0.6762411
PTGS2	Model 1	hapAGC	one	1.743583	0.0213423	0.4181798	-2.424588	6.089808	0.3347417	0.6762411
PTGS2	Model 1	hapAGC	zero	-0.4525221	0.0112428	0.6867296	-2.622098	1.765391	0.3347417	0.6762411
TLR4	Model 1	hapAAGGCCAA	one	-1.834344	0.0179806	0.3034233	-5.233588	1.686829	0.231392	0.6762411
TLR4	Model 1	hapAAGGCCAA	zero	0.6021228	0.0120012	0.6170346	-1.73662	2.996529	0.231392	0.6762411
TLR4	Model 1	hapAGAAAGCAA	one	1.922603	0.0192936	0.3238623	-1.859612	5.850582	0.2453256	0.6762411
TLR4	Model 1	hapAGAAAGCAA	zero	-0.5095931	0.0114054	0.6542915	-2.708941	1.739472	0.2453256	0.6762411
TLR4	Model 1	hapAGAAAGCGG	one	-2.734138	0.0243022	0.2542576	-7.25844	2.010877	0.209035	0.6762411
TLR4	Model 1	hapAGAAAGCGG	zero	0.3797155	0.0109215	0.7286502	-1.74615	2.551577	0.209035	0.6762411
TLR4	Model 1	hapAGAGAGCAA	one	2.82357	0.0361197	0.4409525	-4.203961	10.36664	0.4082657	0.6762411
TLR4	Model 1	hapAGAGAGCAA	zero	-0.2531117	0.0107059	0.8129212	-2.324317	1.862014	0.4082657	0.6762411
TLR4	Model 1	hapAGAGAGCGG	one	2.740255	0.0276207	0.3279394	-2.673777	8.455459	0.2706004	0.6762411
TLR4	Model 1	hapAGAGAGCGG	zero	-0.3039648	0.0106262	0.7745642	-2.35886	1.794177	0.2706004	0.6762411
VEGFA	Model 1	hapAAACAAAGGAG	one	2.649828	0.024861	0.2930628	-2.232047	7.775472	0.2373849	0.6762411
VEGFA	Model 1	hapAAACAAAGGAG	zero	-0.3908224	0.0108614	0.7185259	-2.488889	1.752386	0.2373849	0.6762411
VEGFA	Model 1	hapCTAACGAAAG	one	2.807737	0.0311734	0.374609	-3.285642	9.285023	0.3142073	0.6762411
VEGFA	Model 1	hapCTAACGAAAG	zero	-0.4065717	0.0106698	0.7026717	-2.467684	1.698097	0.3142073	0.6762411
VEGFA	Model 1	hapCTACAAAAG	one	-2.001684	0.0261313	0.4392431	-6.894434	3.148183	0.4140165	0.6762411
VEGFA	Model 1	hapCTACAAAAG	zero	0.1971271	0.0109349	0.8571137	-1.927449	2.367728	0.4140165	0.6762411
VEGFA	Model 1	hapCTACAAAAGGAG	one	-1.389586	0.0200079	0.4844713	-5.181728	2.554217	0.4336433	0.6762411
VEGFA	Model 1	hapCTACAAAAGGAG	zero	0.2547567	0.0112085	0.8204696	-1.923641	2.481539	0.4336433	0.6762411
VEGFA	Model 1	hapCTACAAAGGG	one	-3.781682	0.0293853	0.1898573	-9.166732	1.92262	0.1646024	0.6762411
VEGFA	Model 1	hapCTACAAAGGG	zero	0.30789	0.0107481	0.7749215	-1.783076	2.443371	0.1646024	0.6762411
VEGFA	Model 1	hapCTACCGAGAAA	one	-2.452453	0.0301029	0.4096564	-8.041328	3.476091	0.3887226	0.6762411
VEGFA	Model 1	hapCTACCGAGAAA	zero	0.1644543	0.0107528	0.8785753	-1.92444	2.297839	0.3887226	0.6762411
VEGFA	Model 1	hapCTACCGAGAAG	one	2.260041	0.0171276	0.1922479	-1.115798	5.75113	0.1001839	0.6762411
VEGFA	Model 1	hapCTACCGAGAAG	zero	-0.9373817	0.0119034	0.429012	-3.221782	1.400941	0.1001839	0.6762411
VEGFA	Model 1	hapCTGACGGAAAA	one	-3.990304	0.0285742	0.1544424	-9.219481	1.540087	0.1454937	0.6762411
VEGFA	Model 1	hapCTGACGGAAAA	zero	0.2218356	0.0108117	0.8376499	-1.879575	2.368252	0.1454937	0.6762411
ACE	Model 2	hapTGCAGAGAAAAGGAAGA	one	-0.6564012	0.0557968	0.9060684	-10.94762	10.82411	0.9648784	0.6810906
ACE	Model 2	hapTGCAGAGAAAAGGAAGA	zero	-0.9043176	0.0147252	0.5374272	-3.723433	1.997346	0.9648784	0.6810906
ACE	Model 3	hapACCAGAGGAAAGAAAGA	one	-3.76404	0.0241741	0.1128034	-8.217399	0.9053997	0.1856585	0.6909698
ACE	Model 3	hapACCAGAGGAAAGAAAGA	zero	-0.1763744	0.016083	0.91262	-3.273939	3.020387	0.1856585	0.6909698
ACE	Model 3	hapTGCAGAGAGGGAGTGG	one	3.15157	0.044693	0.4876716	-5.499728	12.59488	0.3543682	0.6909698
ACE	Model 3	hapTGCAGAGAGGGAGTGG	zero	-1.105836	0.0147389	0.4507491	-3.921793	1.792654	0.3543682	0.6909698
ACE	Model 3	hapTGCAGAGAGGGAGTGG	one	-5.309111	0.0356985	0.1267937	-11.70795	1.553473	0.1704784	0.6909698
ACE	Model 3	hapTGCAGAGAGGGAGTGG	zero	-0.3610739	0.0150294	0.8098524	-3.253334	2.61765	0.1704784	0.6909698
ACE	Model 3	hapwaste	one	-0.6346776	0.0150653	0.6726583	-3.525786	2.343071	0.4166655	0.6909698
ACE	Model 3	hapwaste	zero	-2.108409	0.0182159	0.2423486	-5.541731	1.449706	0.4166655	0.6909698
ADRB2	Model 3	hapAGAC	one	1.349854	0.0123754	0.2788676	-1.078854	3.838191	0.0393928	0.6909698
ADRB2	Model 3	hapAGAC	zero	-1.66475	0.0130907	0.1999971	-4.155675	0.8909115	0.0393928	0.6909698
ADRB2	Model 3	hapAGAG	one	-3.033892	0.0317549	0.332181	-8.884947	3.192894	0.3050971	0.6909698
ADRB2	Model 3	hapAGAG	zero	0.2858146	0.010798	0.7915927	-1.814308	2.430858	0.3050971	0.6909698
ADRB2	Model 3	hapGGAC	one	-2.501022	0.0171231	0.1394052	-5.718849	0.8266297	0.0658192	0.6909698
ADRB2	Model 3	hapGGAC	zero	0.829167	0.0114289	0.4701497	-1.404315	3.113244	0.0658192	0.6909698

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
AGT	Model 3	hapAAGCGAAGA	one	-0.6065392	0.0120882	0.6148713	-2.933731	1.776447	0.4272572	0.6909698
AGT	Model 3	hapAAGCGAAGA	zero	0.5132527	0.0131787	0.6977594	-2.049748	3.143318	0.4272572	0.6909698
AGT	Model 3	hapAGAAGGGGA	one	1.03113	0.0159778	0.52099	-2.083725	4.245074	0.355011	0.6909698
AGT	Model 3	hapAGAAGGGGA	zero	-0.6171924	0.0118583	0.6017276	-2.900403	1.719705	0.355011	0.6909698
AGT	Model 3	hapwaste	one	1.478276	0.0190409	0.4410747	-2.239039	5.336941	0.3109325	0.6909698
AGT	Model 3	hapwaste	zero	-0.5800685	0.0112902	0.606473	-2.755902	1.64445	0.3109325	0.6909698
AGTR1	Model 3	hapAAGAAAAAAAGAAGA	one	-3.739374	0.0330607	0.2492878	-9.779056	2.704623	0.2328604	0.6909698
AGTR1	Model 3	hapAAGAAAAAAAGAAGA	zero	0.1740406	0.0106065	0.8698071	-1.886921	2.278295	0.2328604	0.6909698
AGTR1	Model 3	hapAAGGAGGGGAGAAGG	one	-2.053805	0.0260964	0.4266863	-6.937603	3.086288	0.3978497	0.6909698
AGTR1	Model 3	hapAAGGAGGGGAGAAGG	zero	0.1875473	0.0107692	0.8619098	-1.904974	2.324706	0.3978497	0.6909698
ALOX15	Model 3	hapAAAGAACAAAGA	one	2.721684	0.021781	0.2179167	-1.571222	7.20182	0.146101	0.6909698
ALOX15	Model 3	hapAAAGAACAAAGA	zero	-0.7065197	0.01123	0.5279431	-2.868128	1.503194	0.146101	0.6909698
ALOX15	Model 3	hapAAGAACAGCAGA	one	-0.9748773	0.0134823	0.4676261	-3.557335	1.676731	0.3166184	0.6909698
ALOX15	Model 3	hapAAGAACAGCAGA	zero	0.6120852	0.0127231	0.6316066	-1.865841	3.15258	0.3166184	0.6909698
ALOX15	Model 3	hapTAAAAGGCAG	one	4.691245	0.0340677	0.1787018	-2.070881	11.9203	0.1466162	0.6909698
ALOX15	Model 3	hapTAAAAGGCAG	zero	-0.5187899	0.0107977	0.6301132	-2.601991	1.608967	0.1466162	0.6909698
EDN1	Model 3	hapAGAC	one	-0.660702	0.0105602	0.5303261	-2.69566	1.416814	0.0580134	0.6909698
EDN1	Model 3	hapAGAC	zero	1.780607	0.0151228	0.2434615	-1.191922	4.842561	0.0580134	0.6909698
EDN1	Model 3	hapAGGC	one	0.2361156	0.0115189	0.8378173	-2.00152	2.524844	0.4213578	0.6909698
EDN1	Model 3	hapAGGC	zero	-0.8195496	0.0133491	0.5377286	-3.380835	1.809633	0.4213578	0.6909698
EDN1	Model 3	hapCAGA	one	1.323256	0.0175867	0.4549469	-2.109771	4.876679	0.2831814	0.6909698
EDN1	Model 3	hapCAGA	zero	-0.7928985	0.0117754	0.4991758	-3.056319	1.523368	0.2831814	0.6909698
EDN1	Model 3	hapwaste	one	-3.864855	0.0403229	0.3285638	-11.17008	4.041142	0.3265215	0.6909698
EDN1	Model 3	hapwaste	zero	0.1129805	0.0107249	0.9161713	-1.969478	2.239676	0.3265215	0.6909698
GRK4	Model 3	hapACAGGAGCAAGAAGAGAAG	one	1.025615	0.0169355	0.5469673	-2.27268	4.435227	0.4155963	0.6909698
GRK4	Model 3	hapACAGGAGCAAGAAGAGAAG	zero	-0.461382	0.0114651	0.6867748	-2.673194	1.800694	0.4155963	0.6909698
GRK4	Model 3	hapACAGGAGCAAGAAGGGAAG	one	1.875443	0.0247879	0.4536796	-2.95571	6.947106	0.3804094	0.6909698
GRK4	Model 3	hapACAGGAGCAAGAAGGGAAG	zero	-0.3909959	0.0108929	0.7191848	-2.495071	1.758483	0.3804094	0.6909698
GRK4	Model 3	hapACGGGAACAAAACAGACGA	one	-3.162524	0.0292858	0.2727625	-8.564389	2.558475	0.2583861	0.6909698
GRK4	Model 3	hapACGGGAACAAAACAGACGA	zero	0.2144492	0.0108485	0.8435034	-1.893874	2.368081	0.2583861	0.6909698
GRK4	Model 3	hapTGGAGTAAGGAACAAGAAG	one	-2.546266	0.0258877	0.3193355	-7.367613	2.526022	0.2973928	0.6909698
GRK4	Model 3	hapTGGAGTAAGGAACAAGAAG	zero	0.2396428	0.0109555	0.8271002	-1.889805	2.41531	0.2973928	0.6909698
GRK4	Model 3	hapTGGAGTAAGGAACAGGAAG	one	-2.024784	0.0169209	0.2269894	-5.220785	1.278987	0.1921638	0.6909698
GRK4	Model 3	hapTGGAGTAAGGAACAGGAAG	zero	0.3491916	0.0115093	0.7620505	-1.889118	2.638566	0.1921638	0.6909698
GRK4	Model 3	hapwaste	one	0.5297157	0.0134445	0.6944306	-2.08471	3.213949	0.4538782	0.6909698
GRK4	Model 3	hapwaste	zero	-0.5789965	0.0122142	0.6345966	-2.930813	1.8298	0.4538782	0.6909698
PTGS1	Model 3	hapGAGAGGGGCAG	one	0.6669495	0.0131775	0.6140596	-1.899738	3.300791	0.3587494	0.6909698
PTGS1	Model 3	hapGAGAGGGGCAG	zero	-0.7008979	0.0125072	0.5739919	-3.105494	1.763372	0.3587494	0.6909698
PTGS1	Model 3	hapGGGAGGGCAGG	one	-2.940361	0.0248176	0.2294341	-7.548521	1.897487	0.1950704	0.6909698
PTGS1	Model 3	hapGGGAGGGCAGG	zero	0.3079382	0.0108234	0.776412	-1.797527	2.458545	0.1950704	0.6909698
PTGS1	Model 3	hapGGGAGGGCAGG	one	0.5384821	0.0122978	0.6624277	-1.855849	2.991225	0.38972	0.6909698
PTGS1	Model 3	hapGGGAGGGCAGG	zero	-0.7245476	0.0132371	0.5828856	-3.267049	1.88478	0.38972	0.6909698
PTGS1	Model 3	hapGGGGGGAGCAGA	one	-3.907135	0.0538725	0.459593	-13.53611	6.794167	0.4572594	0.6909698
PTGS1	Model 3	hapGGGGGGAGCAGA	zero	0.0466725	0.0104569	0.964417	-1.982932	2.118303	0.4572594	0.6909698
PTGS1	Model 3	hapGGGGGGGGCAG	one	-2.391609	0.0193531	0.2113021	-6.024683	1.381918	0.1600341	0.6909698
PTGS1	Model 3	hapGGGGGGGGCAG	zero	0.5303994	0.0114487	0.6441405	-1.700291	2.81171	0.1600341	0.6909698
PTGS2	Model 3	hapAGC	one	1.468129	0.0209568	0.4869297	-2.615188	5.722658	0.3779364	0.6909698
PTGS2	Model 3	hapAGC	zero	-0.5009942	0.0112378	0.6550219	-2.668575	1.714858	0.3779364	0.6909698

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
TLR4	Model 3	hapAAGGCGCCAA	one	-1.917031	0.0180271	0.2831985	-5.322038	1.610434	0.233374	0.6909698
TLR4	Model 3	hapAAGGCGCCAA	zero	0.5205113	0.0120085	0.6655976	-1.817746	2.914455	0.233374	0.6909698
TLR4	Model 3	hapAGAAAGGCAA	one	2.225128	0.0192067	0.2521474	-1.55155	6.146687	0.1641589	0.6909698
TLR4	Model 3	hapAGAAAGGCAA	zero	-0.6606802	0.0113406	0.5590085	-2.844358	1.572078	0.1641589	0.6909698
TLR4	Model 3	hapAGAAAGGC GG	one	-2.667222	0.0244945	0.2699929	-7.229614	2.119545	0.2383866	0.6909698
TLR4	Model 3	hapAGAAAGGC GG	zero	0.271913	0.010871	0.8028037	-1.841963	2.431312	0.2383866	0.6909698
TLR4	Model 3	hapAGAGAGGCAA	one	2.676724	0.0362108	0.465876	-4.357855	10.2287	0.4208339	0.6909698
TLR4	Model 3	hapAGAGAGGCAA	zero	-0.3295441	0.0107005	0.7577813	-2.398117	1.78287	0.4208339	0.6909698
TLR4	Model 3	hapAGAGAGGC GG	one	1.964851	0.0272287	0.4750163	-3.334087	7.554261	0.4024284	0.6909698
TLR4	Model 3	hapAGAGAGGC GG	zero	-0.3083112	0.0106192	0.7712788	-2.361778	1.788343	0.4024284	0.6909698
VEGFA	Model 3	hapAAACAAAGGAG	one	2.548381	0.024484	0.3042964	-2.256483	7.589442	0.2361966	0.6909698
VEGFA	Model 3	hapAAACAAAGGAG	zero	-0.4589027	0.0108482	0.6716602	-2.553011	1.680207	0.2361966	0.6909698
VEGFA	Model 3	hapCTAACGGAAG	one	2.71614	0.0313505	0.3928556	-3.405348	9.225565	0.3253002	0.6909698
VEGFA	Model 3	hapCTAACGGAAG	zero	-0.4430543	0.0106132	0.6757581	-2.492604	1.649576	0.3253002	0.6909698
VEGFA	Model 3	hapCTACAAAGAAG	one	-1.995757	0.0262732	0.4430853	-6.914708	3.183127	0.432573	0.6909698
VEGFA	Model 3	hapCTACAAAGAAG	zero	0.1112582	0.0108495	0.9183886	-1.995097	2.262884	0.432573	0.6909698
VEGFA	Model 3	hapCTACAAAGGAG	one	-1.598022	0.0198363	0.4169216	-5.350323	2.303035	0.3832087	0.6909698
VEGFA	Model 3	hapCTACAAAGGAG	zero	0.2213857	0.0112059	0.8435986	-1.95579	2.446908	0.3832087	0.6909698
VEGFA	Model 3	hapCTACAAAGGGG	one	-3.79825	0.0295963	0.191053	-9.219928	1.947229	0.1737685	0.6909698
VEGFA	Model 3	hapCTACAAAGGGG	zero	0.2292008	0.0107019	0.8306509	-1.851249	2.35375	0.1737685	0.6909698
VEGFA	Model 3	hapCTACCAGAGAAA	one	-2.274562	0.0305854	0.4520704	-7.960711	3.762876	0.448221	0.6909698
VEGFA	Model 3	hapCTACCGAGAAA	zero	0.0649429	0.0107171	0.9517076	-2.015012	2.18905	0.448221	0.6909698
VEGFA	Model 3	hapCTACCGAGAAG	one	2.275536	0.0168973	0.1832992	-1.056167	5.719426	0.0809576	0.6909698
VEGFA	Model 3	hapCTACCGAGAAG	zero	-1.057693	0.0118361	0.3692039	-3.326578	1.264441	0.0809576	0.6909698
VEGFA	Model 3	hapCTGACGGAAAA	one	-4.131084	0.0292565	0.1496115	-9.473733	1.526875	0.1478193	0.6909698
VEGFA	Model 3	hapCTGACGGAAAA	zero	0.1579624	0.0107909	0.883738	-1.938105	2.298832	0.1478193	0.6909698
AGTR1	Model 2	hapAAGAAAAGAATCGGGG	one	-0.0739813	0.0423151	0.9860493	-8.027095	8.566857	0.9952045	0.6943287
AGTR1	Model 2	hapAAGAAAAGAATCGGGG	zero	-0.0997584	0.0106384	0.9252721	-2.161206	2.005123	0.9952045	0.6943287
GRK4	Model 1	hapACAGGAGCAAGAAGAGAAG	one	0.9660431	0.0167649	0.5664594	-2.297643	4.33875	0.4701237	0.6945009
GRK4	Model 1	hapACAGGAGCAAGAAGAGAAG	zero	-0.3516231	0.0115545	0.7605424	-2.582949	1.930811	0.4701237	0.6945009
ADRB2	Model 3	hapGC GC	one	0.5252486	0.0133526	0.6948929	-2.071441	3.190792	0.4760529	0.7037304
ADRB2	Model 3	hapGC GC	zero	-0.5797575	0.0126894	0.6468981	-3.021911	1.923896	0.4760529	0.7037304
ACE	Model 3	hapACCAGGAAGGGAGAAGA	one	-2.737328	0.0348586	0.4260968	-9.160544	4.140071	0.520422	0.7205139
ACE	Model 3	hapACCAGGAAGGGAGAAGA	zero	-0.5273632	0.0146893	0.7189525	-3.350403	2.378135	0.520422	0.7205139
ADRB2	Model 3	hapGGGG	one	-0.4498785	0.0118312	0.7032073	-2.731769	1.885545	0.5557767	0.7205139
ADRB2	Model 3	hapGGGG	zero	0.365715	0.0133495	0.784561	-2.226256	3.026399	0.5557767	0.7205139
AGT	Model 3	hapGGGCAGGGAG	one	-0.8739254	0.0217798	0.687021	-5.016339	3.449147	0.702333	0.7205139
AGT	Model 3	hapGGGCAGGGAG	zero	0.0002889	0.011154	0.9997934	-2.162135	2.210507	0.702333	0.7205139
AGT	Model 3	hapGGGCAGGGAG	one	-0.9118596	0.0197721	0.6432502	-4.678333	3.00344	0.618778	0.7205139
AGT	Model 3	hapGGGCAGGGAG	zero	0.1722463	0.0115885	0.881972	-2.077325	2.473496	0.618778	0.7205139
AGTR1	Model 3	hapAAGAAGGGAGAAGA	one	0.8740679	0.0172141	0.6132795	-2.472549	4.335523	0.4981265	0.7205139
AGTR1	Model 3	hapAAGAAGGGAGAAGA	zero	-0.3952357	0.0115274	0.7312595	-2.620396	1.88077	0.4981265	0.7205139
AGTR1	Model 3	hapAAGGAGGGAGAAGAAGA	one	-0.5036033	0.0135644	0.7098176	-3.11393	2.177052	0.658789	0.7205139
AGTR1	Model 3	hapAAGGAGGGAGAAGAAGA	zero	0.1662792	0.0122902	0.8924955	-2.217733	2.608415	0.658789	0.7205139
ALOX15	Model 3	hapAAAAAGGC GAG	one	1.987595	0.0342695	0.5658932	-4.63761	9.07308	0.5577615	0.7205139
ALOX15	Model 3	hapAAAAAGGC GAG	zero	-0.0829204	0.0107259	0.9383679	-2.161484	2.039802	0.5577615	0.7205139
ALOX15	Model 3	hapAAAGAAGCAGA	one	-1.685552	0.0311623	0.5855275	-7.510595	4.506355	0.5969173	0.7205139
ALOX15	Model 3	hapAAAGAAGCAGA	zero	0.0281531	0.0109567	0.9795089	-2.097034	2.199472	0.5969173	0.7205139

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
ALOX15	Model 3	hapAAAGAGGCGAG	one	-1.292598	0.0306058	0.6708617	-7.039588	4.809681	0.6798756	0.7205139
ALOX15	Model 3	hapAAAGAGGCGAG	zero	-0.0312677	0.0106114	0.976495	-2.088937	2.069644	0.6798756	0.7205139
ALOX15	Model 3	hapAGAGAGGCGAG	one	-1.43332	0.0303478	0.6343817	-7.125175	4.607361	0.6454528	0.7205139
ALOX15	Model 3	hapAGAGAGGCGAG	zero	-0.0287796	0.0106601	0.9784641	-2.095854	2.081937	0.6454528	0.7205139
ALOX15	Model 3	hapwaste	one	-0.3984547	0.012513	0.749742	-2.811483	2.074485	0.7099181	0.7205139
ALOX15	Model 3	hapwaste	zero	0.1176276	0.0125657	0.9254812	-2.317981	2.613966	0.7099181	0.7205139
EDN1	Model 3	hapAAGA	one	1.22852	0.0250989	0.6267279	-3.630718	6.332776	0.5655109	0.7205139
EDN1	Model 3	hapAAGA	zero	-0.3006642	0.0110886	0.7860202	-2.444082	1.889846	0.5655109	0.7205139
EDN1	Model 3	hapCGGC	one	1.348219	0.0365498	0.7141391	-5.65805	8.874805	0.6836531	0.7205139
EDN1	Model 3	hapCGGC	zero	-0.1798407	0.0107105	0.8665684	-2.253439	1.937747	0.6836531	0.7205139
PTGS1	Model 3	hapGGGGGAGGCAG	one	-1.271698	0.0306097	0.675949	-7.020617	4.832676	0.7054164	0.7205139
PTGS1	Model 3	hapGGGGGAGGCAG	zero	-0.0984017	0.010703	0.9267296	-2.172262	2.019422	0.7054164	0.7205139
PTGS2	Model 3	hapCAA	one	-1.96954	0.041248	0.6297323	-9.582872	6.284853	0.6372415	0.7205139
PTGS2	Model 3	hapCAA	zero	0.0157067	0.0107811	0.98838	-2.075505	2.151577	0.6372415	0.7205139
PTGS2	Model 3	hapCGA	one	0.4267587	0.0157317	0.7866806	-2.622501	3.571502	0.6517949	0.7205139
PTGS2	Model 3	hapCGA	zero	1.220899	0.0310206	0.6957377	-4.749908	7.56599	0.6517949	0.7205139
TLR4	Model 3	hapAAGGCCGCAA	one	0.2471539	0.0118641	0.8352214	-2.057017	2.605532	0.61184	0.7205139
TLR4	Model 3	hapAAGGCCGCAA	zero	-0.496239	0.0136877	0.7163479	-3.13017	2.20931	0.61184	0.7205139
TLR4	Model 3	hapAGAGAGGGAG	one	0.7339376	0.0210119	0.727898	-3.33028	4.969025	0.6316907	0.7205139
TLR4	Model 3	hapAGAGAGGGAG	zero	-0.3479731	0.0112865	0.7575021	-2.52818	1.881	0.6316907	0.7205139
TLR4	Model 3	hapGAGGCCGCAA	one	-0.6894504	0.0180583	0.7017174	-4.142938	2.888458	0.6714471	0.7205139
TLR4	Model 3	hapGAGGCCGCAA	zero	0.1203968	0.0113316	0.9154574	-2.078726	2.368907	0.6714471	0.7205139
TLR4	Model 3	hapwaste	one	-0.6151843	0.0172461	0.7205606	-3.918421	2.801615	0.6865621	0.7205139
TLR4	Model 3	hapwaste	zero	0.1111934	0.011315	0.9217804	-2.084537	2.356162	0.6865621	0.7205139
VEGFA	Model 3	hapCTGACGGAAAG	one	-0.8476228	0.0183669	0.6431342	-4.353471	2.78673	0.6470699	0.7205139
VEGFA	Model 3	hapCTGACGGAAAG	zero	0.0667323	0.0115442	0.9539302	-2.17198	2.356675	0.6470699	0.7205139
VEGFA	Model 3	hapCTACCGGGAAA	one	1.020887	0.0393379	0.7963045	-6.475217	9.11781	0.7414787	0.733862
VEGFA	Model 3	hapCTACCGGGAAA	zero	-0.2816488	0.0104781	0.7878497	-2.308653	1.787414	0.7414787	0.733862
VEGFA	Model 3	hapwaste	one	-0.24295	0.0115386	0.8330778	-2.473653	2.038775	0.7446541	0.733862
VEGFA	Model 3	hapwaste	zero	0.1763199	0.0131396	0.8933728	-2.370594	2.789676	0.7446541	0.733862
ALOX15	Model 1	hapAAAGAACGACA	one	-1.899732	0.0302344	0.5259778	-7.544094	4.089213	0.5120363	0.7409802
ALOX15	Model 1	hapAAAGAACGACA	zero	0.169658	0.0110317	0.8779078	-1.972932	2.359079	0.5120363	0.7409802
AGT	Model 3	hapAGGCAGGGA	one	-0.6430805	0.0219673	0.7690555	-4.830112	3.728161	0.7859821	0.7423164
AGT	Model 3	hapAGGCAGGGA	zero	-0.0239769	0.0110611	0.9827081	-2.168073	2.167109	0.7859821	0.7423164
AGTR1	Model 3	hapwaste	one	-0.1009949	0.0104254	0.9228072	-2.12156	1.961282	0.7770478	0.7423164
AGTR1	Model 3	hapwaste	zero	-0.447579	0.0163468	0.783821	-3.586596	2.793638	0.7770478	0.7423164
ALOX15	Model 3	hapAAAGGACAAGA	one	0.8640172	0.0385034	0.8232418	-6.467601	8.770331	0.7847802	0.7423164
ALOX15	Model 3	hapAAAGGACAAGA	zero	-0.206643	0.0106227	0.8456433	-2.262874	1.892847	0.7847802	0.7423164
PTGS2	Model 1	hapCGA	one	0.7329618	0.0157637	0.6432704	-2.331727	3.893816	0.524333	0.7435995
PTGS2	Model 1	hapCGA	zero	1.862741	0.0311078	0.5531194	-4.162306	8.266565	0.524333	0.7435995
ADRB2	Model 3	hapwaste	one	0.4925316	0.0303258	0.8713272	-5.306451	6.64664	0.8366153	0.7439269
ADRB2	Model 3	hapwaste	zero	-0.1456957	0.0107168	0.891809	-2.22121	1.973875	0.8366153	0.7439269
ALOX15	Model 3	hapAAAGAACGAG	one	-0.6022456	0.0268939	0.8223282	-5.705923	4.777669	0.8517472	0.7439269
ALOX15	Model 3	hapAAAGAACGAG	zero	-0.0877502	0.0107997	0.9352291	-2.180369	2.049635	0.8517472	0.7439269
GRK4	Model 3	hapACAGGAGCAAGAACGGACGA	one	-0.4479858	0.0196537	0.819342	-4.209865	3.46163	0.8267667	0.7439269
GRK4	Model 3	hapACAGGAGCAAGAACGGACGA	zero	0.0080707	0.0112763	0.9942911	-2.177969	2.242963	0.8267667	0.7439269
PTGS1	Model 3	hapwaste	one	-0.0767693	0.0118574	0.9483713	-2.372222	2.272655	0.8182076	0.7439269
PTGS1	Model 3	hapwaste	zero	-0.3697511	0.0126594	0.7698758	-2.811364	2.133201	0.8182076	0.7439269

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
PTGS2	Model 3	hapwaste	one	0.4433904	0.0309408	0.88633	-5.466766	6.723046	0.8533279	0.7439269
PTGS2	Model 3	hapwaste	zero	-0.1467209	0.0108163	0.8920485	-2.241292	1.992729	0.8533279	0.7439269
VEGFA	Model 3	hapCTGACGGAAAGG	one	-0.5828081	0.0239379	0.8071427	-5.139483	4.19275	0.8325119	0.7439269
VEGFA	Model 3	hapCTGACGGAAAGG	zero	-0.0670512	0.0108154	0.9505618	-2.163115	2.073919	0.8325119	0.7439269
ACE	Model 3	hapACCAGAGGAAAGATGGG	one	-0.5621237	0.0288091	0.8449077	-6.021283	5.214154	0.9295313	0.7501846
ACE	Model 3	hapACCAGAGGAAAGATGGG	zero	-0.8261123	0.015128	0.5835748	-3.723488	2.158458	0.9295313	0.7501846
ACE	Model 3	hapTGCAGAGGAAAGGGAAAAGA	one	-0.4712586	0.0392992	0.9043496	-7.849647	7.49791	0.9213558	0.7501846
ACE	Model 3	hapTGCAGAGGAAAGGGAAAAGA	zero	-0.8598231	0.0146703	0.5562407	-3.66983	2.032153	0.9213558	0.7501846
ACE	Model 3	hapTGCAGAGGAGGGAGAAGA	one	-0.7423292	0.0159936	0.6414081	-3.805484	2.418366	0.9060684	0.7501846
ACE	Model 3	hapTGCAGAGGAGGGAGAAGA	zero	-0.9725954	0.0184553	0.5965212	-4.490581	2.674971	0.9060684	0.7501846
AGT	Model 3	hapAGGAGGGAG	one	0.0197194	0.0145963	0.9892247	-2.801122	2.922426	0.9377308	0.7501846
AGT	Model 3	hapAGGAGGGAG	zero	-0.1109337	0.0121824	0.9274228	-2.467752	2.302835	0.9377308	0.7501846
AGTR1	Model 3	hapAAGAAAAGAATCGGGG	one	-0.4736915	0.0410778	0.9080009	-8.172567	7.870664	0.927574	0.7501846
AGTR1	Model 3	hapAAGAAAAGAATCGGGG	zero	-0.0954912	0.0106293	0.9284005	-2.155285	2.007665	0.927574	0.7501846
ALOX15	Model 3	hapAAAGAACGAGG	one	0.0638345	0.0153764	0.9669046	-2.906826	3.125386	0.9054577	0.7501846
ALOX15	Model 3	hapAAAGAACGAGG	zero	-0.1386069	0.0119081	0.9072971	-2.442324	2.21951	0.9054577	0.7501846
GRK4	Model 3	hapACAGGAGCAAGAACGA	one	-0.0238346	0.0123242	0.9845721	-2.409816	2.420482	0.8761683	0.7501846
GRK4	Model 3	hapACAGGAGCAAGAACGA	zero	-0.2476715	0.0130197	0.8489837	-2.760956	2.330572	0.8761683	0.7501846
ACE	Model 3	hapTGCAGAGAAAAGGAAGA	one	-1.108193	0.0540915	0.8368196	-11.05582	9.951992	0.9612384	0.760049
ACE	Model 3	hapTGCAGAGAAAAGGAAGA	zero	-0.8420324	0.0147668	0.5670214	-3.670769	2.069771	0.9612384	0.760049
ACE	Model 1	hapACCAGGAAGGGAGAAGA	one	-2.217132	0.0354896	0.5276906	-8.787582	4.826619	0.5943549	0.775836
ACE	Model 1	hapACCAGGAAGGGAGAAGA	zero	-0.3328872	0.0147132	0.8207599	-3.165985	2.583099	0.5943549	0.775836
ADRB2	Model 1	hapGGGG	one	-0.363408	0.011818	0.7580981	-2.644754	1.971397	0.5814561	0.775836
ADRB2	Model 1	hapGGGG	zero	0.4050346	0.0134819	0.7643759	-2.213328	3.093508	0.5814561	0.775836
AGT	Model 1	hapGGGCAGGGAG	one	-0.9849336	0.0220759	0.6539835	-5.177749	3.393278	0.6399115	0.775836
AGT	Model 1	hapGGGCAGGGAG	zero	0.0951871	0.0111447	0.9319847	-2.067508	2.305643	0.6399115	0.775836
AGTR1	Model 1	hapAAGGAGGGGAGAAGA	one	-0.5112992	0.0136555	0.7074526	-3.138733	2.187406	0.5980111	0.775836
AGTR1	Model 1	hapAAGGAGGGGAGAAGA	zero	0.2958651	0.0123237	0.8105938	-2.09766	2.747907	0.5980111	0.775836
ALOX15	Model 1	hapAAAGAGCGAG	one	-1.219679	0.0299722	0.6823059	-6.855326	4.756949	0.6649475	0.775836
ALOX15	Model 1	hapAAAGAGCGAG	zero	0.0770698	0.0106597	0.9423997	-1.992115	2.18994	0.6649475	0.775836
ALOX15	Model 1	hapAGAGAGCGAG	one	-1.215246	0.029957	0.6832525	-6.848372	4.75853	0.67194	0.775836
ALOX15	Model 1	hapAGAGAGCGAG	zero	0.0640301	0.0107102	0.9523546	-2.014574	2.186729	0.67194	0.775836
EDN1	Model 1	hapAAGA	one	1.054277	0.0252711	0.6782284	-3.829043	6.185559	0.638172	0.775836
EDN1	Model 1	hapAAGA	zero	-0.2027698	0.0110983	0.8549225	-2.350149	1.991832	0.638172	0.775836
TLR4	Model 1	hapAAGGCGCAA	one	0.2712649	0.0119365	0.8205093	-2.047356	2.64477	0.6783592	0.775836
TLR4	Model 1	hapAAGGCGCAA	zero	-0.3464295	0.0137653	0.8010112	-2.999086	2.378768	0.6783592	0.775836
TLR4	Model 1	hapAGAGAGGGAG	one	0.7826175	0.020981	0.7102993	-3.277713	5.013398	0.6438217	0.775836
TLR4	Model 1	hapAGAGAGGGAG	zero	-0.2634934	0.0113449	0.8161485	-2.456726	1.979053	0.6438217	0.775836
TLR4	Model 1	hapwaste	one	-0.6381862	0.0171952	0.7097259	-3.931084	2.76758	0.6235786	0.775836
TLR4	Model 1	hapwaste	zero	0.2447612	0.0113599	0.829657	-1.96252	2.501739	0.6235786	0.775836
VEGFA	Model 1	hapCTACCGGGAAA	one	1.53697	0.0401209	0.7039	-6.141591	9.843715	0.66142	0.775836
VEGFA	Model 1	hapCTACCGGGAAA	zero	-0.2304177	0.010501	0.8261678	-2.262855	1.844284	0.66142	0.775836
VEGFA	Model 1	hapCTGACGGAAAG	one	-0.8386588	0.018519	0.6493716	-4.373345	2.826682	0.6204374	0.775836
VEGFA	Model 1	hapCTGACGGAAAG	zero	0.1551789	0.0115418	0.8931563	-2.08504	2.446653	0.6204374	0.775836
AGT	Model 1	hapGGGCAGGGAG	one	-0.6729751	0.0201546	0.7376688	-4.520131	3.329193	0.6990904	0.7804379
AGT	Model 1	hapGGGCAGGGAG	zero	0.1851709	0.0115822	0.8731283	-2.063488	2.48546	0.6990904	0.7804379
ALOX15	Model 1	hapwaste	one	-0.3066081	0.0126907	0.8088523	-2.755735	2.204201	0.7043952	0.7804379
ALOX15	Model 1	hapwaste	zero	0.2267433	0.012547	0.8567888	-2.207946	2.722048	0.7043952	0.7804379

gene	analysis	haplotype	num_haplos	estimate	stderr	p	min95	max95	p_int	q
ALOX15	Model 1	hapAAAGGACAAGA	one	1.298168	0.0390346	0.7411455	-6.162744	9.352289	0.7201098	0.7855743
ALOX15	Model 1	hapAAAGGACAAGA	zero	-0.1292499	0.0106531	0.9033949	-2.192898	1.977939	0.7201098	0.7855743
ACE	Model 1	hapACCAGAGGAAGATGGG	one	-0.2294438	0.0290074	0.9368981	-5.743522	5.607213	0.8992465	0.7910535
ACE	Model 1	hapACCAGAGGAAGATGGG	zero	-0.6125364	0.0151211	0.684585	-3.514843	2.377073	0.8992465	0.7910535
ACE	Model 1	hapTGCAGAGAAAAGGAAGA	one	0.5227137	0.0545475	0.9238752	-9.669731	11.86523	0.8222674	0.7910535
ACE	Model 1	hapTGCAGAGAAAAGGAAGA	zero	-0.7211086	0.0146536	0.6214947	-3.53189	2.17157	0.8222674	0.7910535
ACE	Model 1	hapTGCAGAGAAAAGGGAAAAGA	one	-0.2711278	0.0379949	0.9430492	-7.428008	7.439061	0.9240046	0.7910535
ACE	Model 1	hapTGCAGAGAAAAGGGAAAAGA	zero	-0.6360968	0.0146743	0.6637569	-3.453205	2.26321	0.9240046	0.7910535
ADRB2	Model 1	hapwaste	one	0.3447552	0.0300402	0.9088113	-5.392756	6.430221	0.8901857	0.7910535
ADRB2	Model 1	hapwaste	zero	-0.0790667	0.0107583	0.9414048	-2.163929	2.050223	0.8901857	0.7910535
AGT	Model 1	hapAGGAGGGAG	one	0.0919085	0.0146133	0.9498869	-2.734221	3.000153	0.9370942	0.7910535
AGT	Model 1	hapAGGAGGGAG	zero	-0.0403964	0.0122233	0.973637	-2.406688	2.383269	0.9370942	0.7910535
AGT	Model 1	hapAGGCAGGGA	one	-0.4130704	0.0220641	0.8512274	-4.627907	3.988035	0.8437852	0.7910535
AGT	Model 1	hapAGGCAGGGA	zero	0.0401333	0.0111079	0.9711915	-2.114316	2.242002	0.8437852	0.7910535
AGTR1	Model 1	hapAAGAAAGAACATCGGGG	one	0.4268073	0.0417007	0.9186721	-7.454786	8.979634	0.9085593	0.7910535
AGTR1	Model 1	hapAAGAAAGAACATCGGGG	zero	-0.0605146	0.0106606	0.9547303	-2.127024	2.049628	0.9085593	0.7910535
AGTR1	Model 1	hapwaste	one	-0.019389	0.0104573	0.9852095	-2.047732	2.050956	0.8043663	0.7910535
AGTR1	Model 1	hapwaste	zero	-0.3270777	0.0165726	0.8433326	-3.512608	2.963623	0.8043663	0.7910535
ALOX15	Model 1	hapAAAGAACGCAGG	one	-0.0828552	0.0154296	0.9571682	-3.059268	2.984943	0.9342973	0.7910535
ALOX15	Model 1	hapAAAGAACGCAGG	zero	0.0581315	0.0119439	0.961203	-2.256994	2.428092	0.9342973	0.7910535
ALOX15	Model 1	hapAAAGAACGCAG	one	-0.4147733	0.0270268	0.8778093	-5.552683	5.002637	0.8796761	0.7910535
ALOX15	Model 1	hapAAAGAACGCAG	zero	0.0045287	0.0108408	0.9966678	-2.097908	2.152114	0.8796761	0.7910535
EDN1	Model 1	hapCGGC	one	0.8751388	0.0369747	0.8137479	-6.176589	8.456871	0.8004768	0.7910535
EDN1	Model 1	hapCGGC	zero	-0.081469	0.0107353	0.9394984	-2.161881	2.04318	0.8004768	0.7910535
GRK4	Model 1	hapACAGGAGCAAGAACGGACGA	one	-0.3819829	0.0198156	0.84689	-4.17676	3.563074	0.826493	0.7910535
GRK4	Model 1	hapACAGGAGCAAGAACGGACGA	zero	0.0790375	0.0113029	0.9442881	-2.11367	2.320863	0.826493	0.7910535
PTGS1	Model 1	hapGGGGGAGGCAG	one	-0.4034527	0.0305098	0.894612	-6.184568	5.733908	0.9109274	0.7910535
PTGS1	Model 1	hapGGGGGAGGCAG	zero	-0.05555709	0.0107446	0.958751	-2.138304	2.071488	0.9109274	0.7910535
PTGS1	Model 1	hapwaste	one	0.0557595	0.0118854	0.9626014	-2.248098	2.413915	0.7531691	0.7910535
PTGS1	Model 1	hapwaste	zero	-0.3484892	0.0127541	0.7843611	-2.80866	2.173955	0.7531691	0.7910535
PTGS2	Model 1	hapCAA	one	-0.9823038	0.0399032	0.8046585	-8.431287	7.072644	0.8016575	0.7910535
PTGS2	Model 1	hapCAA	zero	0.0483392	0.0108237	0.9643956	-2.051744	2.19345	0.8016575	0.7910535
PTGS2	Model 1	hapwaste	one	0.5822079	0.0309021	0.8510264	-5.328936	6.862436	0.8367357	0.7910535
PTGS2	Model 1	hapwaste	zero	-0.0769887	0.0108656	0.9435052	-2.182466	2.073807	0.8367357	0.7910535
TLR4	Model 1	hapGAGGCAGCAA	one	-0.3419927	0.018293	0.8514844	-3.851796	3.295933	0.8188655	0.7910535
TLR4	Model 1	hapGAGGCAGCAA	zero	0.1014768	0.0113275	0.9286712	-2.096427	2.348723	0.8188655	0.7910535
VEGFA	Model 1	hapCTGACGGAAGG	one	-0.4315014	0.024059	0.8573939	-5.017659	4.376095	0.8611101	0.7910535
VEGFA	Model 1	hapCTGACGGAAGG	zero	-0.0043254	0.0108239	0.9968123	-2.103339	2.139694	0.8611101	0.7910535
VEGFA	Model 1	hapwaste	one	-0.1637311	0.0115485	0.887193	-2.398106	2.121795	0.769011	0.7910535
VEGFA	Model 1	hapwaste	zero	0.2166059	0.0132245	0.8700676	-2.34758	2.848123	0.769011	0.7910535
ACE	Model 1	hapTGCAGAGAACGGAGAAGA	one	-0.6774652	0.0160546	0.6720862	-3.754132	2.497553	0.9751635	0.8135054
ACE	Model 1	hapTGCAGAGAACGGAGAAGA	zero	-0.6171488	0.0182786	0.734921	-4.114551	3.00782	0.9751635	0.8135054
GRK4	Model 1	hapACAGGAGCAAGAACGAA	one	-0.045183	0.0123933	0.9709182	-2.443875	2.412488	0.9969648	0.8220217
GRK4	Model 1	hapACAGGAGCAAGAACGAA	zero	-0.0506731	0.0130416	0.969006	-2.573115	2.537076	0.9969648	0.8220217

Model	Analysis	Exposure (m)	Percent difference in LVM (95% CI)		p value
			>150	Referent	
	Adjusted only for height and weight	101-150	2.0 (0.3, 3.9)		0.03
1	Adjusted only for height and weight	50-100	1.8 (0.0, 3.6)		0.05
1	Adjusted only for height and weight	<50	2.4 (0.9, 3.9)		0.002
2	All covariates except center, blood pressure	101-150	2.5 (0.9, 4.1)		0.002
2	All covariates except center, blood pressure	50-100	2.3 (0.7, 3.9)		0.005
2	All covariates except center, blood pressure	<50	2.9 (1.5, 4.3)		<0.001
3	All covariates except blood pressure	101-150	1.2 (-0.4, 2.8)		0.14
3	All covariates except blood pressure	50-100	0.6 (-1.0, 2.3)		0.48
3	All covariates except blood pressure	<50	1.6 (0.2, 3.1)		0.03
4	Full model	101-150	1.2 (-0.3, 2.7)		0.13
4	Full model	50-100	0.7 (-0.9, 2.3)		0.40
4	Full model	<50	1.7 (0.3, 3.1)		0.02
5	Full model + center/race interaction	101-150	1.2 (-0.4, 2.7)		0.14
5	Full model + center/race interaction	50-100	0.7 (-0.9, 2.3)		0.41
5	Full model + center/race interaction	<50	1.6 (0.2, 3.1)		0.02

Supplemental Material, Table 4: Difference in left ventricular mass associated with proximity to traffic, Multi-Ethnic Study of Atherosclerosis and Air Pollution, 2002, n=3827. This is a re-parameterization of the results described in Table 2 of Van Hee, et al. Exposure to traffic and left ventricular mass and function: The multi-ethnic study of atherosclerosis. *American Journal of Respiratory and Critical Care Medicine* 2009;179:827-34. This analysis uses log-LVM as the outcome, adjusted for height and weight, instead of LVM index as the outcome. The full model includes height, weight, age, sex, race/ethnicity, household income, highest educational attainment level, antihypertensive medication use, low-density lipoprotein and high-density lipoprotein cholesterol, lipid-lowering medication use, physical activity, weekly alcohol consumption, current smoking and pack-year history of smoking, hours per week of secondhand smoke exposure, diabetes status by fasting blood glucose criteria, use of diabetes medications, center, and systolic and diastolic blood pressure. Abbreviations: LVM = left ventricular mass